

GenCore version 5.1.6  
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CM nucleic - nucleic search, using sw model

Run on: April 10, 2004, 01:54:35 / Search time 8415.96 seconds

(without alignments)  
11057.263 Million cell updates/sec

Title: US-09-508-377-10\_COPY\_1058\_3204

Perfect score: 2147  
Sequence: 1 cgcagcttcacaccccgcc.....tcagatactatgaccagag 2147

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

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40: em\_hcg\_hum:\*  
41: em\_hcg\_other:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	1197	55.8	1852	8 AF064562	AF064562 Hordeum v
4	243	11.3	2853	8 AR340173	AR340173 Sequence
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6	238.2	11.1	2549	8 BT008928	BT008928 Triticum
7	235	10.9	2726	8 AF38432	AF38432 Triticum
8	235	10.9	2970	8 TASBA2	TASBA2 Triticum
9	233.4	10.9	2970	8 AF286319	AF286319 Triticum
10	201.4	9.4	2554	8 AF064560	AF064560 Hordeum v
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14	135.8	6.3	3015	6 E14723	E14723 Rice mRNA
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17	116	5.4	2304	6 AX654742	AX654742 Sequence
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#### ALIGNMENTS

RESULT 1  
AX031271  
LOCUS AX031271 11463 bp DNA  
DEFINITION Sequence 10 from Patent WO9914314.  
ACCESSION AX031271  
VERSION AX031271.1 GI:10278603  
KEYWORDS  
SOURCE Aegilops tauschii  
ORGANISM Aegilops tauschii  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticaceae; Aegilops.

JOURNAL Patent: WO 9914314-A 10 25-MAR-1999;  
GOODMAN FIELDER LTD (AU) ; LI ZHONGYI (AU) ; MORELL MATTHEW (AU) ;  
RAHMAN SADEOUR (AU) ; UNIV AUSTRALIAN (AU) ; COMM SCI ENT IND RES  
ORG (AU) ; GROUPE LIMBRAIN PACIFIC PTY L (AU)  
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ORIGIN

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Matches 2147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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1058 CGCAGCCTTCACCCCGCCGACACGTTGCTCCCTTCATCGCTTCAATTAA 1117  
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QY 121 CTGGCTACCTCAATCACTACGCGGGGATGGGAGCGTTGCGCGGTGTCGGGCGGCACTCTCG 180  
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QY 841 TGTGAGCTTTCAGCCCGTGTGCTTCTTGGGCGGCACTGAAAAATCAGATGATGCA 900  
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RESULT 2  
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LOCUS Aegilops tauschii starch branching enzyme ita gene, complete cds.  
DEFINITION AF38431  
ACCESSION AF38431  
VERSION AF38431.1 GI:13447949

KEYWORDS  
SOURCE  
ORGANISM  
Aegilops tauschii  
Aegilops tauschii  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Aegilops.  
1 (bases 1 to 11475)  
Rahman, S., Regina, A., Li, Z., Mukai, Y., Yamamoto, M.,  
Kohar, Hashemi, B., Abrahams, S. and Morell, M.K.  
Comparison of starch-branching enzyme genes reveals evolutionary  
relationships among isoforms. Characterization of a gene for  
starch-branching enzyme ita from the wheat genome donor Aegilops  
tauschii  
Plant Physiol. 125 (3), 1314-1324 (2001)

JOURNAL  
MEDLINE  
PUBMED  
11240316  
2 (bases 1 to 11475)  
Rahman, S., Regina, A., Li, Z., Sharon, A. and Morell, M.K.  
Direct Submission  
Submitted (18-JAN-2001) Plant Industry, CSIRO, Clunies Ross,  
Canberra, ACT 2601, Australia  
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ORIGIN  
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DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

1852 bp. DNA. linear. PLN 10-NOV-1998  
Hordeum vulgare cultivar Bomi starch branching enzyme Iia (sbeIIa)  
gene, nuclear gene encoding plastid protein, partial cds.  
AF064562.1 GI:3851525

Hordeum vulgare subsp. vulgare  
Hordeum vulgare subsp. vulgare  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Pooidae; Triticeae; Hordeum.  
1 (bases 1 to 1852)  
Sun, C., Sathish, P., Ahlandsberg, S. and Jansson, C.  
The two genes encoding starch-branching enzymes Iia and Iib are  
differentially expressed in barley  
Plant Physiol. 118 (1), 37-49 (1998)  
9733524

2 (bases 1 to 1852)  
Sun, C., Sathish, P., Ahlandsberg, S. and Jansson, C.  
Direct Submision  
Submitted (11-MAY-1998) Stockholm University, Biochemistry,  
Stockholm S-10691, Sweden  
Location/Qualifiers

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Db 392 CCAAAGAGTTAAGAGACTAGTCGTGGGGGAGAAACCGCGAGTTGTCCTCCAAAACGAGAG 451
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Db 452 ATGGGCGAGAAATATACGAGATTGACCCACACTGAAGATTGTTGGAGCCATCTTACT 511
QY 1218 ACCGCTAATGC 1228
Db 512 ACCGATACCGC 522

RESULT 5
TAU6376 2853 bp mRNA linear PLN 18-OCT-1996
LOCUS Triticum aestivum 1.4-alpha-D-glucan
DEFINITION 6-alpha-D-(1,4-alpha-D-glucanotransferase mRNA, complete cds.
ACCESSION U66376
VERSION U66376.1 GI:1620661
KEYWORDS Triticum aestivum (bread wheat)
SOURCE Triticum aestivum
ORGANISM Triticum aestivum
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
1 (bases 1 to 2853)
REFERENCE 1 (bases 1 to 2853)
AUTHORS Kroege, C., Loerz, H. and Luetzelcke, S.
TITLE Direct Submission
JOURNAL Submitted (08-AUG-1996) University of Hamburg, Institute of General
Botany, Centre of Applied Molecular Biology, AMP II, Ohnhorststr.
16, Hamburg 22609, Germany
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Db 392 CCAAAGAGTTAAGAGACTAGTCGTGGGGGAGAAACCGCGAGTTGTCCTCCAAAACGAGAG 451
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QY 1218 ACCGCTAATGC 1228
Db 512 ACCGATACCGC 522

RESULT 6
BT008928 2549 bp mRNA linear PLN 20-JUN-2003
LOCUS Triticum aestivum clone wdel.f.pk002.98.fis, full insert mRNA
DEFINITION sequence.
ACCESSION BT008928
VERSION BT008928.1 GI:32128479
KEYWORDS FLI CDNA.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
1 (bases 1 to 2549)
REFERENCE 1 (bases 1 to 2549)
AUTHORS Tingey, S.V., Wolters, P., Powell, W., Dolan, M., Miao, G.-H.,
Carlier, N.R., Hanafey, M.K. and Hainey, C.F.
TITLE Direct Submission
JOURNAL Submitted (20-JUN-2003) Crop Genetics, E. I. DuPont de Nemours and
Company, 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104,
USA
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Matches 243; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 978 AGATACCTGAAGATATCCAGAGCAAAACGGCGAAGTGAACATGACAGAGGGGAGCTGCAG 1037
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Db 463 ATGGGCGAGAAATATACGAGATTGACCCACACTGAAGATTGTTGGAGCCATCTTACT 522
QY 1218 ACCGCTAATGC 1228
Db 523 ACCGATACCGC 533
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RESULT 7  
LOCUS AF338432 2726 bp mRNA linear PLN 27-MAR-2001  
DEFINITION Triticum aestivum starch branching enzyme I1a variant mRNA,  
complete cds.  
ACCESSION AF338432  
VERSION AF338432.1 GI:13447951  
KEYWORDS Triticum aestivum (bread wheat)  
SOURCE Triticum aestivum  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Triticum.  
1 (bases 1 to 2726)  
Rahman, S., Regina, A., Li, Z., Mukai, Y., Yamamoto, M.,  
Kosar-Hademi, B., Abrahams, S. and Morell, M.K.  
Comparison of starch-branching enzyme genes reveals evolutionary  
relationships among isoforms Characterization of a gene for  
starch-branching enzyme I1a from the wheat genome donor Aegilops  
tauschii  
Plant Physiol. 125 (3), 1314-1324 (2001)  
JOURNAL MEDLINE 21140316  
PUBMED 11244112  
REFERENCE 2 (bases 1 to 2726)  
AUTHORS Rahman, S., Regina, A., Li, Z., Abrahams, S. and Morell, M.K.  
TITLE Direct Submission  
JOURNAL Submitted (18-JAN-2001) Plant Industry, CSIRO, Clunies Ross,  
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Query Match 10.9%; Score 235; DB 8; Length 2726;  
Best Local Similarity 96.0%; Pred. No. 4.1e-46;  
Matches 241; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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2Y 1038 AGAACTCAATCTTCAGAACGAGCTCAGGCGATTGTGGAACAATCATCTGATGTGTA 1097  
2b AAAAATTGATCTTCAGAACGAGCTCAGGCGATTGTGGAACAATCATCTGATGTGTA 319  
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2b CCAAGGAGTTAAGAACTAGTGTGGGGGAGAAACCGCGAGTTGTCCCAAAACGAGAG 379  
1158 ATGGCAGAAAAATATTCGAGATTGACCCCAACTGAAGATTTCGGAAGCATCTTGACT 1217

Db 360 ATGGCAGAAAAATATTCGAGATTGACCCCAACTGAAGATTTCGGAAGCATCTTGACT 439  
QY 1218 ACCGGTAATGC 1228  
Db 440 ACCGATACAGC 450

RESULT 8  
LOCUS TASB2 2970 bp mRNA linear PLN 27-FEB-1997  
DEFINITION T.aestivum mRNA for starch branching enzyme II.  
ACCESSION Y11282  
VERSION Y11282.1 GI:1885343  
KEYWORDS 1,4-alpha-glucan branching enzyme; sbe2 gene; starch branching  
enzyme II.  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Triticum.  
1  
Nair, R.B., Baga, M., Scoles, G.J., Kartha, K.K. and Chibbar, R.N.  
Isolation, characterization and expression analysis of a starch  
branching enzyme II cDNA from wheat  
Plant Sci.  
2 (bases 1 to 2970)  
Chibbar, R.N.  
Direct Submission  
Submitted (14-FEB-1997) R.N. Chibbar, Plant Biotechnology  
Institute, National Research Council of Canada, 110 Gymnasium  
place, Saskatoon, Saskatchewan S7N 0W9, CANADA  
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Query Match      10.9%   Score 235;   DB 8;   Length 2970;
Best Local Similarity 96.0%   Pred. No. 4.2e-46;
Matches 241;   Conservative 0;   Mismatches 10;   Indels 0;   Gaps 0;

QY  978  AGATACCTGGAAGATATCGAGGAGCAAAACGCGGGAAGTGAACATGACAGAGGGGGACTGCAG 1037
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Db   512  CCAAGAGGTTAAGAACTAGTCGTGGGGGGGAAACCGCGATTTGCCCAAAACAGAGG 571
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RESULT 9
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LOCUS        Triticum aestivum starch branching enzyme 2 (Sbe2) mRNA, complete
DEFINITION   cds.
VERSION      AF286319
KEYWORDS     Triticum aestivum starch branching enzyme 2 (Sbe2) mRNA, complete
SOURCE       Triticum aestivum (bread wheat)
ORGANISM     Triticum aestivum
REFERENCE    1. Triticum aestivum (bread wheat)
AUTHORS      Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE        Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
             Pooidae; Triticeae; Triticum.
             1 (bases 1 to 2970)
             McCue K.F., Hurkman, W.J., Tanaka, C.K. and Anderson, O.D.
             Starch Branching Enzymes Sbe1 and Sbe2 from Wheat (Triticum
             aestivum cv. Cheyenne): Molecular Characterization, Developmental
             Expression, and Homolog Assignment by Differential PCR
             Plant Mol. Biol. Rep. 20 (2), 191-192 (2002)
             2 (bases 1 to 2970)
             McCue K.F. and Anderson, O.D.
             Direct Submission
             Submitted (11-JUN-2000) United States Department of Agriculture,
             Agricultural Research Service, 800 Buchanan Street, Albany, CA
             94710-1105, USA

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Query Match 9.4%; Score 201.4; DB 8; Length 2554;  
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Matches 211; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

2y 1002 AACGCGGGAAGTGAACATGACAGGGGGAGCTGCAGAGAACTTCAATCTTCAGAACCA 1061  
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2y 1122 TGGGGGGAAGACCGCGAGTTTCCCAAAACGAGAGTGGGAGAAATATCGGATTCG 1181  
125 TTGGGGGGAAGACCGCGAGTTTCCCAAAACGAGAGTGGGAGAAATATCGGATTCG 184  
2y 1182 ACCCAACTGAAGATTTCCGAGCCATCTTGAATACCGGATATGC 1228  
185 ACCCAACTGAAGATTTCCGAGCCATCTTGAATACCGGATATGC 231

## RESULT 11

AY357072 3094 bp DNA linear PLN 02-SEP-2003  
LOCUS Triticum aestivum cultivar Yumai-18 starch branching enzyme Ila  
DEFINITION (SbeIIa) gene, promoter region and partial cds.  
ACCESSION AY357072  
VERSION AY357072.1 GI:34329814

## SOURCE

ORGANISM Triticum aestivum (bread wheat)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Pooidae; Triticaceae; Triticum.  
1 (bases 1 to 3094)  
Miao,H.M., Han,J.F. and Fleming,J.E.  
Investigation of endosperm-specific promoters in wheat  
Unpublished  
2 (bases 1 to 3094)  
Miao,H.M., Han,J.F. and Fleming,J.E.  
Direct Submission  
Submitted (31-Jun-2003) Institute of Biotechnology, Henan Academy  
of Agricultural Sciences, No.1 Nongye Road, Zhengzhou, Henan  
Province 450002, China  
Location/Qualifiers  
1..3094

FEATURES  
Source

## ORIGIN

Query Match 6.9%; Score 149; DB 8; Length 3094;  
Best Local Similarity 100.0%; Pred. No. 4.5e-25;  
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCCAGCTTCACCCCGCCGACACCTGTGCTCCCTTCATCGCTTCATTAATA 60  
DB 2946 CGCCAGCTTCACCCCGCCGACACCTGTGCTCCCTTCATCGCTTCATTAATA 3005  
Qy 61 TCTCCATCACTCGGATTCGCGCTGCACTTCGCGCGGGTGAAGAGATCGGCGCA 120  
DB 3006 TCTCCATCACTCGGATTCGCGCTGCACTTCGCGCGGGTGAAGAGATCGGCGCA 3065  
Qy 121 CTGGCTGACTCACTCACTACGCGGGGATG 149  
DB 3066 CTGGCTGACTCACTCACTACGCGGGGATG 3094

## RESULT 12

OSUN00286/c 159683 bp DNA linear HTG 14-NOV-2003  
LOCUS Oryza sativa (japonica cultivar-group) chromosome 4 clone  
DEFINITION OSUNBa0042115, \*\*\* SEQUENCING IN PROGRESS \*\*\*; 11 ordered pieces.  
ACCESSION AL731641  
VERSION AL731641.3 GI:32490295  
KEYWORDS HTG; HTGS PHASB2.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Erihartoideae; Oryzaceae; Oryza.

## REFERENCE

1  
Feng,Q., Zhang,Y., Hao,P., Wang,S., Fu,G., Huang,Y., Li,Y., Zhu,J.,  
Liu,Y., Hu,X., Jia,P., Zhang,Y., Zhao,Q., Ying,K., Yu,S., Tang,Y.,  
Weng,Q., Zhang,L., Lu,Y., Mu,J., Lu,Y., Zhang,L.S., Yu,Z., Fan,D.,  
Liu,X., Lu,T., Li,C., Wu,Y., Sun,T., Lei,H., Li,T., Hu,H., Guan,J.,  
Wu,M., Zhang,R., Zhou,B., Chen,Z., Chen,L., Jin,Z., Wang,R.,  
Yin,H., Cai,Z., Ren,S., Lv,G., Gu,W., Zhu,G., Tu,Y., Hu,Q.,  
Zhang,Y., Chen,J., Kang,H., Chen,X., Shao,C., Sun,Y., Hu,Q.,  
Zhang,X., Zhang,W., Wang,L., Ding,C., Sheng,H., Gu,J., Chen,S.,  
Ni,L., Zhu,F., Chen,W., Lan,L., Lai,Y., Cheng,Z., Gu,M., Jiang,J.,  
Li,J., Hong,G., Xue,Y. and Han,B.  
Sequence and analysis of rice chromosome 4  
Nature 420 (6913), 316-320 (2002)

TITLE  
JOURNAL MEDLINE  
PUBMED  
12447439  
2  
Fu,G., Wang,S.Y., Ren,S.X., Lv,G., Lin,W., Gu,W.Q., Zhu,G.F.,







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PN JP 1998004970-A/2
PD 13-JAN-1998
PF 24-JUN-1996 JP 1996162983
PI BABA TADASHI, KAWASAKI TSUTOMU, ICHIKAWA NORIO PC
C12N15/09,A01H5/00,C07H21/04,C12N5/10,C12N9/10,(C12N15/09, PC
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CC topology: Linear;
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FT /issue_type='Immature Seed'
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Matches 167; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
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DB 162 GGCAGAGCAACGCTTAAGGTGTGGCTGAGAGACAAATTGATTTGAGAAGTATTC 221
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DB 222 AGACATTGAGGAAATGTGACTGAGGGGTGATCAAAATGCTGATGAACCAACTGTGGA 281
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DB 282 GGATTAACCAAGATTATCCACCAACGAGAGATGCGGAGAAATATCAAAATTGACCC 341
QY 1186 AACACTGAAGATTTTCGAGCCATCTTGACTACCGGTA 1224
DB 342 AATGCTGAAGATTTCGAAACCATCTTGACTACCGATA 380
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LOCUS E14723 3015 bp DNA linear PAT 28-JUL-1999
DEFINITION Rice mRNA for branching enzyme-4, complete cds.
VERSION E14723.1 GI:5709406
KEYWORDS JP 1998004970-A/1.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Euphorbiaceae; Oryzaceae; Oryza.
1 (bases 1 to 3015)
Baba,T., Kawasaki,T. and Ichikawa,N.
NEW RICE GENE FOR STARCH-BRANCHING ENZYME
Parent: JP 1998004970-A.1.13-JAN-1998;
MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO:KK, MITSUI PETROCHEM IND LTD
OS Oryza sativa (rice)
PN JP 1998004970-A/1
PD 13-JAN-1998
PF 24-JUN-1996 JP 1996162983
PI BABA TADASHI, KAWASAKI TSUTOMU, ICHIKAWA NORIO PC
C12N15/09,A01H5/00,C07H21/04,C12N5/10,C12N9/10,(C12N15/09, PC
C12R1:91),
PC (C12N5/10,C12R1:91),(C12N9/10,C12R1:19);

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CC topology: Linear;
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Best Local Similarity 76.3%; Pred. No. 7.5e-22;
Matches 167; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
QY 1006 GGGGAAGTGAACATGACAGGGGGGAGCTGCAGAGAACTTCATCTTCAGAACCCGACTCA 1065
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QY 1066 GGGCATTGTGGAAACAATCACTGATGTGTAAACCAAGAGTTAAGAACTGATGTGG 1125
DB 509 AACACTGGAAGATTTTCGAGCCATCTTGACTACCGGTA 1185
QY 1126 GGAGAAACCGGAGATTGTCCAAAACCGAGATGCGGAGAAATATCGAGATTGACCC 1185
DB 569 GGATTAACCAAGATTATCCACCAACGAGATGCGGAGAAATATCAAAATTGACCC 628
QY 1186 AACACTGAAGATTTTCGAGCCATCTTGACTACCGGTA 1224
DB 629 AATGCTGAAGATTTCGAAACCATCTTGACTACCGATA 667
RESULT 15
LOCUS AB023498 3015 bp mRNA linear PLN 04-AUG-1999
DEFINITION Oryza sativa mRNA for starch branching enzyme rbe4, complete cds.
VERSION AB023498.1 GI:5689137
KEYWORDS starch branching enzyme rbe4.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Euphorbiaceae; Oryzaceae; Oryza.
1 (sites)
Mizuno,K., Tachibana,M., Kobayashi,E., Kawasaki,T., Funane,K.,
Kobayashi,M. and Baba,T.
Molecular cloning and expression analysis of a novel member of
starch branching enzyme isoform in developing rice seeds
Unpublished
2 (bases 1 to 3015)
Mizuno,K. and Baba,T.
Direct Submission
Submitted (09-FEB-1999) Kouichi Mizuno, University of Tsukuba,
Institute of Agricultural and Forest Engineering, 1-1-1 Tennoudai,
Tsukuba, Ibaraki 305-8572, Japan
(E-mail:koumomo@tsukuba.ac.jp, Tel:81-298-53-4656,
Fax:81-298-55-2203)
REFERENCE
JOURNAL
1 (bases 1 to 3015)
Baba,T. and Mizuno,K.
NEW RICE GENE FOR STARCH-BRANCHING ENZYME
Submitted (09-FEB-1999) Kouichi Mizuno, University of Tsukuba,
Institute of Agricultural and Forest Engineering, 1-1-1 Tennoudai,
Tsukuba, Ibaraki 305-8572, Japan
(E-mail:koumomo@tsukuba.ac.jp, Tel:81-298-53-4656,
Fax:81-298-55-2203)
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HNAVYDKWIEELKQDEYKMGDIYHLLTRNRESEKVTYASHDQALVGDXTIAFL  
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## ORIGIN

Query Match 6.3%; Score 135.8; DB 8; Length 3015;  
Best Local Similarity 76.3%; Pred. No. 7.5e-22;  
Matches 167; Conservative 0; Mismatches 52; Indels 0; Gaps 0;  
QY 1006 GGCGAAGTGAACATGACAGGGGGAGTGCAGAGAAACTTCAATCTTCAGAACCGACTCA 1065  
DB 449 GGCGAAGTGAACATGACAGGGGGAGTGCAGAGAAACTTCAATCTTCAGAACCGACTCA 508  
QY 1066 GGCGAAGTGAACATGACAGGGGGAGTGCAGAGAAACTTCAATCTTCAGAACCGACTCA 1125  
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QY 1126 GGAAGAACCGGAGTGTGCCAAACCAAGAGATGGGCAAGAAATATACGAGATTGACCC 1185  
DB 569 GGAAGAACCGGAGTGTGCCAAACCAAGAGATGGGCAAGAAATATACGAGATTGACCC 628  
QY 1186 AACACTGAAGATTTTCGAGAGCCATCTTGACTACCGGTA 1224  
DB 629 AATGCTGAAGATTTTCGAGAGCCATCTTGACTACCGGTA 667

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Job time : 8425.29 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

DM nucleic - nucleic search, using sw model

Run on: April 10, 2004, 01:51:55 ; Search time 840.046 Seconds  
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Perfect score: 2147  
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Scoring table: IDENTITY\_NUC  
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Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 2: geneseqn1990s:\*
- 3: geneseqn2000s:\*
- 4: geneseqn2001s:\*
- 5: geneseqn2001bs:\*
- 6: geneseqn2002s:\*
- 7: geneseqn2003as:\*
- 8: geneseqn2003bs:\*
- 9: geneseqn2003cs:\*
- 10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	2127	99.1	11473	2	AA34650 Search br
2	2124	98.9	11475	5	Aah78338 Nucleotid
3	235	10.9	2726	5	Aah78337 Nucleotid
4	177.6	8.3	226	5	Aah78351 Nucleotid
5	164.2	7.6	217	5	Aah78353 Nucleotid
6	159.2	7.4	228	5	Aah78352 Nucleotid
7	155.8	6.3	3015	2	AAV05639 Rice type
8	117.8	5.5	2655	7	ADA71289 Rice gene
9	116	5.4	2304	9	ADC08218 Rice DNA
10	84.4	3.9	2968	5	Aah78342 Nucleotid
11	84.4	3.9	3039	6	ABK15494 Wheat sta
12	82.2	3.8	3962	5	Aah78341 Partial s
13	82.2	3.8	8381	5	Aah78343 Partial s
14	79.4	3.7	2919	5	AAQ73750 Rice star
15	78.6	3.7	2307	9	ADC07807 Rice DNA
16	73.8	3.4	23449	3	AA235393 Maize amy
17	61.6	2.9	2640	6	AAV70961 DNA encod
18	59.8	2.8	2577	6	AB212532 Arabidops
19	59.8	2.8	2715	3	AAc45939 Arabidops
20	59.8	2.8	3331	2	AA142632 Class A s
21	58.8	2.7	3090	2	AAV38720 Full leng
22	58.4	2.7	2087	2	AA169737 Corn star
23	58.4	2.7	2165	2	AA169736 Corn star

24	58.4	2.7	2665	2	AA169729 Placmid p
25	58.4	2.7	2725	2	AAV29757 Zea mays
26	58.4	2.7	2913	2	AAV38719 Full leng
27	58.2	2.7	2531	2	AA17267 Class A s
28	58.2	2.7	2563	5	ABK50301 Potato cd
29	58.2	2.7	2576	2	AA172636 Class A s
30	58.2	2.7	2578	2	AA172631 Class A s
31	58.2	2.7	3033	2	AA142630 Class A s
32	58.2	2.7	3074	2	AA142630 Class A s
33	57.2	2.7	262	5	AAH78354 Nucleotid
34	56.6	2.6	3003	2	AA142634 Class A s
35	55	2.6	2418	6	AB213067 Arabidops
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37	55	2.6	2529	2	AA142637 Class A s
38	53.8	2.5	507	2	AA169733 Corn star
39	52.6	2.4	349	3	AA169733 Corn star
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41	50.2	2.3	335913	5	AA161371 Soybean 2
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43	47.8	2.2	2975	2	AA142635 Class A s
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45	45.2	2.1	2000	7	ADA71938 Rice gene

## ALIGNMENTS

RESULT 1	AA34650	ID	AA34650 standard; DNA, 11473 BP.
AC	AA34650;	XX	
DT	17-OCT-2003 (revised)	XX	
DT	05-JUL-1999 (first entry)	XX	
DE	Starch branching enzyme II (SBE II) gene sequence.	XX	
XX	Starch biosynthetic pathway; cereal plant; enzyme; SBE; SSS; DBE; GBS;	XX	
KM	starch branching enzyme; starch soluble synthase; debranching enzyme;	XX	
KM	endosperm; wheat; barley; granule-bound synthase; glutenn; starch;	XX	
KM	grain softness protein I; bacterial isomylase; glycogen synthase;	XX	
KM	WBBE I-D4 gene; ss.	XX	
OS	Aegilops tauschii.	XX	
PN	WO9914314-A1.	XX	
PD	25-MAR-1999.	XX	
PF	11-SEP-1998; 98WO-AU000743.	XX	
PR	12-SEP-1997; 97AU-00009108.	XX	
PR	20-MAR-1998; 98AU-00002509.	XX	
XX	(CSIR ) COMMONWEALTH SCI & IND RES ORG.	XX	
PA	(AUSU ) UNIV AUSTRALIAN NAT.	XX	
PA	(GOOD-) GOODMAN FIELDER LTD.	XX	
PA	(LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.	XX	
PI	L1 Z, Morell M, Rahman S;	XX	
XX	WPI; 1999-229525/19.	XX	
DR	New isolated cereal plant enzyme genes used for, e.g. expression of	XX	
PT	antisense sequences of granule bound synthase.	XX	
XX	Claim 8; Page 75-81; 171pp; English.	XX	
XX	The invention relates to a novel enzyme of starch biosynthetic pathway in	XX	
CC	a cereal plant, where the enzyme is selected from starch branching enzyme	XX	
CC	(SBE) I, SBE II, starch soluble synthase (SSS) I, and debranching enzyme	XX	
CC	(DBE), with the proviso that the enzyme is not SSS I of rice, or SBE I of	XX	



2978 GAGAAATGGGCTCCCTGGAGGCGCATGTTATGTTCTTTAAGTTCCTTAACGAGACACCTTC 3037  
1971 CAATTTATGTTATATGACATATTCACCACTAGCTTACGGAATTCATTAATTAAGCTTA 2030  
3038 CAATTTATGTTATATGACATATTCACCACTAGCTTACGGAATTCATTAATTAAGCTTA 3097  
2031 CTGAAATCTGACGACCTTACTATTAATTTATGATCTGCTTTGACACCTGTTACAGCTTG 2090  
3098 CTGAATCTGACGACCTTACTATTAATTTATGATCTGCTTTGACACCTGTTACAGCTTG 3157  
2091 CAGCATTAGTAGTGACTTCAACAACTTGAATCCAAATGACAGATCTATGACCAAG 2147  
3158 CAGCATTAGTAGTGACTTCAACAACTTGAATCCAAATGACAGATCTATGACCAAG 3214

RESULT 2  
AAH78338 standard; cDNA; 11475 BP.  
AAH78338;  
26-NOV-2001 (first entry)  
Nucleotide sequence of a starch branching enzyme designated F2.  
Wheat; starch branching enzyme; BE1b; SBE; transgenic plant;  
starch biosynthetic pathway; amylopectin; F2; amylose; se.  
Aegilops tauschii.  
MO200162934-A1.  
30-AUG-2001.  
21-FEB-2001; 2001MO-AU000175.  
21-FEB-2000; 2000AU-00005742.  
(CSIR ) COMMONWEALTH SCI & IND RES ORG.  
(GOOD-) GOODMAN FIELDER LTD.  
(LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.  
Morell M, Rahman S;  
WPI; 2001-570635/64.  
Nucleic acids encoding wheat starch branching enzyme 11b, useful for  
altering the amylose and amylopectin content of cereal plants, e.g. wheat  
and barley.  
Example 1; Fig 2; 103pp; English.  
The present sequence encodes a wheat starch branching enzyme of Aegilops  
tauschii, designated F2. A. tauschii is likely to be the ancestral D  
genome donor of wheat. Probes isolated from the present sequence were  
used to identify type II starch branching enzymes (SBEs) in wheat,  
especially BE1b. The BE1b nucleic acids may be used to genetically  
transform cereal plants such as wheat or barley and for altering their  
nutritional content by modulating the starch biosynthetic pathway to vary  
levels of amylopectin and/or amylose produced in the plant

Sequence 11475 BP; 3093 A; 2259 C; 2423 G; 3689 T; 0 U; 11 Other;  
Query Match 98.9%; Score 2124; DB 5; Length 11475;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2146; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

1 CGCGAGCTTCAACCGCGCGGACAGCTTGTCTCCCTTCATCGCTTCAATTAATA 60  
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61 TCTCATCACTCGGCTTCCGCGCTGCAATTCGCGCGGAGTTGATGATCTGGCGCA 120

1118 TCTCATCACTCGGCTTCCGCGCTGCAATTCGCGCGGAGTTGATGATCTGGCGCA 1177  
121 CTGGCTGACTCAATCACTACGCGGGGATGCGAGCTTCGCGGCTCCGCGGACTCTCG 180  
1178 CTGGCTGACTCAATCACTACGCGGGGATGCGAGCTTCGCGGCTCCGCGGACTCTCG 1237  
181 GTGTGGCGCGGCGCGGCGTGGAGTGGCGCGGCGGCTCGGAGCGGAGGCGGCGG 240  
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1358 CTCCCGGCTGCTGCTGCTCTCTCTCTCTGCGCGGCAATGCGCTGTTGAT 1417  
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1478 CTGAACCTGATTTTTCCTCCCGCGGGGAAATGCTTAACTGTCACCCAGGCGCTGCTT 1537  
481 ACCAGGCTTGAATCAATCTCTGTTGATCTGATATATATTTCTGATCTTTCTTC 540  
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780 TGGCTGAGGTTTGAAGCTTCTTCTATAGCATTTGAGTACTGCACTGCTTGTTCAT 839  
1838 TGGCTGAGGTTTGAAGCTTCTTCTATAGCATTTGAGTACTGCACTGCTTGTTCAT 1897  
840 TTGTTAGCCTTGGCCCGGCTGCTGCTTGGGCACTGTAAGATGATGAT 899  
1898 TTGTTAGCCTTGGCCCGGCTGCTGCTTGGGCACTGTAAGATGATGAT 1957  
900 TCTAGCAAGACTTCAACATATATGACCTTGGGCTTGGTGTCTGCTTCAAT 959  
1958 TCTAGCAAGACTTCAACATATATGACCTTGGGCTTGGTGTCTGCTTCAAT 2017  
960 TGTATATTTTTCGCTGCTGATATCTGATATGAGTATGAGGAGCAACGCGGAGGAACA 1019  
2018 TGTATATTTTTCGCTGCTGATATCTGATATGAGTATGAGGAGCAACGCGGAGGAACA 2077  
1020 TGACAGGAGGAGTCAAGCAAACTTCAATCTTCAAGACGACTGAGGCAATTTGAGAA 1079  
2078 TGACAGGAGGAGTCAAGCAAACTTCAATCTTCAAGACGACTGAGGCAATTTGAGAA 2137  
1080 CAATCACTGATGTTAAACCAAGAGTTAAGAACTTGTGTGGGAGAAACCGCGAG 1139  
2138 CAATCACTGATGTTAAACCAAGAGTTAAGAACTTGTGTGGGAGAAACCGCGAG 2197  
1140 TTGTCCCAAAACAGAGAGAGGCGAGAAATATGAGATTTGACCAACATGAAAGAT 1199  
2198 TTGTCCCAAAACAGAGAGAGGCGAGAAATATGAGATTTGACCAACATGAAAGAT 2257

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QY 1200 TTGGAGCCATCTTGACTACCGGTAATCCCTACCCCGCTTGGCTATTGAAATTA 1259
DB 2258 TTGGAGCCATCTTGACTACCGGTAATCCCTACCCCGCTTGGCTATTGAAATTA 2317
QY 1260 GGTCCCTTCATCATGCAAAATTTGGGGAACATCAAAAGAGACAAAGACTAGGACCACTT 1319
DB 2318 GGTCCCTTCATCATGCAAAATTTGGGGAACATCAAAAGAGACAAAGACTAGGACCACTT 2377
QY 1320 TCATACAGATCCCTGCTGCTGCTGAGATATGCTGGAAATGTAATTAATGAGCT 1379
DB 2378 TCATACAGATCCCTGCTGCTGCTGAGATATGCTGGAAATGTAATTAATGAGCT 2437
QY 1380 ACAATTTGCTCAAAATTTGCAATACGAATTAATCTGCTGCAATTAATTAAGAGTG 1439
DB 2438 ACAATTTGCTCAAAATTTGCAATACGAATTAATCTGCTGCAATTAATTAAGAGTG 2497
QY 1440 CAAACTGATGAAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1499
DB 2498 CAAACTGATGAAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2557
QY 1500 ATTCTAGAGGGGGAATCTACCACTTGGGAACTTAAGTTCTTAATCTTGGCCCTTTT 1559
DB 2558 ATTCTAGAGGGGGAATCTACCACTTGGGAACTTAAGTTCTTAATCTTGGCCCTTTT 2617
QY 1560 GTTTTGGGGAACACATTTGCTAATTCGAATGATTTTGGGTATACCTGGGTGATTCGA 1619
DB 2618 GTTTTGGGGAACACATTTGCTAATTCGAATGATTTTGGGTATACCTGGGTGATTCGA 2677
QY 1620 CAGATACAGCGAATPACAAAGAAATTCGTCGCTATTGACCAACATGAAAGTGAATGA 1679
DB 2678 CAGATACAGCGAATPACAAAGAAATTCGTCGCTATTGACCAACATGAAAGTGAATGA 2737
QY 1680 AGCATTTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1739
DB 2738 AGCATTTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2797
QY 1740 TATTATGAAACGCTCCACTATGATGATGATGATGATGATGATGATGATGATGATGAT 1799
DB 2798 TATTATGAAACGCTCCACTATGATGATGATGATGATGATGATGATGATGATGATGAT 2857
QY 1800 TTTTCCCTCTCTTTTTCAGTCTGAAGGATGCTAATTTGCAATCTTATTAAGAA 1859
DB 2858 TTTTCCCTCTCTTTTTCAGTCTGAAGGATGCTAATTTGCAATCTTATTAAGAA 2917
QY 1860 ATTATATCTCTGTTTCCCTATTTTCAGTCTGAAGGATGCTAATTTGCAATCTTATTAAG 1919
DB 2918 ATTATATCTCTGTTTCCCTATTTTCAGTCTGAAGGATGCTAATTTGCAATCTTATTAAG 2977
QY 1920 CTCCCTGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1979
DB 2978 CTCCCTGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3036
QY 1980 GTTAATGATCACTATTCACCACTAGCTTACTGACCTTACCAATTAAGTACTGATGAT 2039
DB 3037 GTTAATGATCACTATTCACCACTAGCTTACTGACCTTACCAATTAAGTACTGATGAT 3096
QY 2040 GACCAAGTACTATAAATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 2099
DB 3097 GACCAAGTACTATAAATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 3156
QY 2100 TAGGTGATCTTCAAAATTTGCAATTCGAATGCAATGCAATGCAATGCAATGCAATG 2147
DB 3157 TAGGTGATCTTCAAAATTTGCAATTCGAATGCAATGCAATGCAATGCAATGCAATG 3204

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XX DE Nucleotide sequence of wheat starch branching enzyme 9 (BE1a).
XX KM wheat, starch branching enzyme; BE1a; BE1b; SBE; transgenic plant;
XX KN starch biosynthetic pathway; amylopectin; amylose; ss.
XX OS Triticum sp.
XX PN WO200162934-A1.
XX PD 30-AUG-2001.
XX PF 21-FEB-2001; 2001WO-AU000175.
XX PR 21-FEB-2000; 2000AU-00005742.
XX PA (CSTR) COMMONWEALTH SCI & IND RES ORG.
XX PA (GOOD-) GOODMAN FIELDER LTD.
XX PA (LIMA-) GRP LIMARAIN PACIFIC PTY LTD.
XX PI Morell M, Rahman S;
XX DR WPI, 2001-570635/64.
XX PT Nucleic acids encoding wheat starch branching enzyme 1b, useful for
XX PT altering the amylose and amylopectin content of cereal plants, e.g. wheat
XX PT and barley.
XX PS Example 1, Fig 1, 103pp; English.
XX CC The present sequence encodes wheat starch branching enzyme 9, designated
XX CC BE1a. The specification describes BE1b. BE1b is a type II starch
XX CC branching enzyme (SBE). The BE1b nucleic acids may be used to
XX CC genetically transform cereal plants such as wheat or barley and for
XX CC altering the nutritional content by modulating the starch biosynthetic
XX CC pathway to vary levels of amylopectin and/or amylose produced in the
XX CC plant
XX SQ Sequence 2726 BP; 726 A; 564 C; 701 G; 735 T; 0 U; 0 Other;

Query Match 10.9%; Score 235; DB 5; Length 2726;
Best Local Similarity 96.0%; Pred. No. 2, 5e-55;
Matches 241; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 978 AGATACCTGAGATATCGAGAGCAACGCGAGGAACTGAAATGATGACAGGGGAGCTGACG 1037
DB 200 AGATACCTGAGATATCGAGAGCAACGCGAGGAACTGAAATGATGACAGGGGAGCTGACG 259
QY 1038 AGAACTTCATCTTCAGAACCGACTCAAGGCAATTTGGAACCAATCACTGATGCTGTA 1097
DB 260 AAAAATTGATCTTCAGAACCGACTCAAGGCAATTTGGAACCAATCACTGATGCTGTA 319
QY 1098 CCAAGAGCTTAAGAACTAGTGTGGGGGAGAAACCGCAAGTGTCCCAAAACGAGAG 1157
DB 320 CCAAGAGCTTAAGAACTAGTGTGGGGGAGAAACCGCAAGTGTCCCAAAACGAGAG 379
QY 1158 ATGGGCAAGAAATATACGAGATGACCCAACTGAAAGATTTTGGAGCATCTTGACT 1217
DB 380 ATGGGCAAGAAATATACGAGATGACCCAACTGAAAGATTTTGGAGCATCTTGACT 439
QY 1218 ACCGATATGC 1228
DB 440 ACCGATATGAC 450

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RESULT 3  
 AAH78337  
 ID AAH78337 standard; cDNA, 2726 BP.  
 XX  
 AC AAH78337;  
 XX  
 DT 26-NOV-2001 (first entry)

RESULT 4  
 AAH78351  
 ID AAH78351 standard; DNA; 226 BP.  
 XX  
 AC AAH78351;  
 XX  
 DT 26-NOV-2001 (first entry)







XX Identifying at least one gene involved in plant resistance or response to  
 PT pathogenic infection for conferring resistance or tolerance to a plant to  
 PI bacterial, fungal or viral infection by determining or detecting plant  
 PT gene expression.

XX Claim 6; SEQ ID NO 4612; 899bp; English.

XX The present invention relates to a method (M1) for identifying genes  
 CC involved in plant resistance or response to pathogenic infection. M1  
 CC comprises identifying a gene whose expression is significantly altered in  
 CC the incompatible interaction of plant gene expression relative to  
 CC the incompatible interaction of the gene in an uninfected plant, in a mutant plant that  
 CC does not express a gene associated with response to pathogenic infection,  
 CC or in a corresponding incompatible or compatible interaction. (M1) is  
 CC useful for conferring resistance to resistance or tolerance to a plant to  
 CC bacterial, fungal or viral infection. The present sequence was used to  
 CC illustrate the invention.

XX Sequence 2655 BP; 714 A; 529 C; 680 G; 732 T; 0 U; 0 Other;

XX Query Match 5.5%; Score 117.8; DB 7; Length 2655;  
 Best Local Similarity 67.1%; Pred. No. 4e-22;  
 Matches 167; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

XX 978 AGATACCTGAAGATATGAGAGGCAACCGGGAAGTGAACATGACAGGGGGACTGCAG 1037  
 DB AGATACCTGAAGATATGAGAGGCAACCGTTCGAGAGGAGAGAGATTCACAGTG 328

XX 1038 AGAACTTCATCTTCGAAACCGACTCGGCGATTGTGAAACATCACTGATGTGTA 1097

XX 329 GCAGAACCAAGCATTAAGAACTGATCAAGACATTAAGAAATGATGATGGGTGCA 388

XX 1098 CCAAGAGATTAAAGAACTGATCGTGGGGGAGAAACCGGAGTTTCCCAAAACAGAG 1157

XX 389 TCAGAGATGCTGATGAGAACCACTGTGAGAGATTAACCAAGATTTCACACACAGAG 448

XX 1158 ATGGGCGAGAAATATATGAGATTGACCAACACTGAAAGATTTTGGAGCCATCTTGACT 1217

XX 449 ATGGGCGAGAAATATATGCAAAATGACCAATGCTGGAAGATTGGAAACCATCTTGACT 508

XX 1218 ACCGCTAAT 1226

XX 509 ACCGCAAT 517

XX Db

XX RESULT 9

XX ADC08218 standard; DNA; 2304 BP.

XX ADC08218;

XX 18-DEC-2003 (first entry)

XX Rice DNA sequence Seq ID523 related to grain filling.

XX plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;  
 KW carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;  
 KW tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;  
 KW wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;  
 KW gene; ds; plant.

XX Oryza sativa.

XX WO200300905-A2.

XX 03-JAN-2003.

XX 21-JUN-2002; 2002WO-IB002450.

XX 22-JUN-2001; 2001US-0300112P.

XX 26-SEP-2001; 2001US-0325277P.

XX 20-DEC-2001; 2001US-0342327P.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;  
 PI Glazebrook J, Katagiri F, Kreps J, Provart N, Riecke D;

XX WPI; 2003-229341/22.

XX P-PsDB; ADC08219.

XX New plant genes encoding polypeptides having an activity involved in or  
 PT associated with the synthesis, metabolism or degradation of carbohydrates  
 PT in the plant grain useful in generating plants having improved  
 PT nutritional properties.

XX Claim 35; SEQ ID NO 523; 130bp; English.

XX This invention, in the area of plant biotechnology, relates to novel  
 CC polynucleotides comprising a nucleotide sequence encoding a protein which  
 CC is involved in or associated with the synthesis, metabolism or  
 CC degradation of carbohydrates in the plant grain and the expression of,  
 CC which is up-regulated during grain filling. The plant is selected from  
 CC corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,  
 CC sugarbeet, wheat, and rice. The invention may be useful for the  
 CC improvement of protein, oil, starch, fibre and moisture content of the  
 CC cereal grains. In addition, carbohydrate levels may be modified to a more  
 CC desirable level using the present invention. The present sequence is a  
 CC DNA sequence encoding a rice protein of the invention. Note: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/publishedpct\_sequences.

XX Sequence 2304 BP; 610 A; 457 C; 620 G; 617 T; 0 U; 0 Other;

XX Query Match 5.4%; Score 116; DB 9; Length 2304;  
 Best Local Similarity 67.2%; Pred. No. 1.2e-21;  
 Matches 164; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

XX 978 AGATACCTGAAGATATGAGAGGCAACCGGGAAGTGAACATGACAGGGGGACTGCAG 1037

XX 287 AGATACCTGAAGATATGAGAGGCAACCTTTTGGAGAGAGAGAGATTCACAGTG 346

XX 1038 AGAACTTCATCTTCGAAACCGACTCGGCGATTGTGAAACATCACTGATGTGTA 1097

XX 347 GCAGAACCAAGCATTAAGAGTGTATCAAGACATGAGAAATGTGACTGAGGGTGTGA 406

XX 1098 CCAAGAGATTAAAGAACTGATCGTGGGGGAGAAACCGGAGTTTCCCAAAACAGAG 1157

XX 407 TCAGAGATGCTGATGAGAACCACTGTGAGAGATTAACCAAGATTATCCACACAGAG 466

XX 1158 ATGGGCGAGAAATATATGAGATTGACCAACACTGAAAGATTTTGGAGCCATCTTGACT 1217

XX 467 ATGGGCGAGAAATATATGCAAAATGACCAATGCTGGAAGATTGGAAACCATCTTGACT 526

XX 1218 ACCG 1221

XX 527 ACCG 530

XX Db

XX RESULT 10

XX AAH78342 standard; cDNA; 2968 BP.

XX AAH78342;

XX 26-NOV-2001 (first entry)

XX Nucleotide sequence of wheat starch branching enzyme (BE11b).

XX wheat; starch branching enzyme; BE11b; SBE; transgenic plant;  
 KW starch biosynthetic pathway; amylopectin; amylose; ss.

XX Triticum sp.

XX WO200162934-A1.

XX 30-AUG-2001.

XX 21-FEB-2001, 2001WO-AU000175.

XX 21-FEB-2000, 2000AU-00005742.

XX (CSIR) COMMONWEALTH SCI & IND RES ORG.

XX (GOOD-) GOODMAN FIELDER LTD.

XX (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.

XX Morell M, Rahman S;

XX WPI; 2001-570635/64.

XX Nucleic acids encoding wheat starch branching enzyme IIb useful for

XX altering the amylose and amylopectin content of cereal plants, e.g. wheat

XX and barley.

XX Claim 6; Fig 9; 103pp; English.

XX The present sequence encodes a wheat starch branching enzyme, designated

XX BBIB, BBIB is a type II starch branching enzyme (SBE). The BBIB

XX nucleic acids may be used to genetically transform cereal plants such as

XX wheat or barley and for altering their nutritional content by modulating

XX the starch biosynthetic pathway to vary levels of amylopectin and/or

XX amylose produced in the plant

XX Sequence 2968 BP; 784 A; 626 C; 796 G; 756 T; 0 U; 6 Other;

XX Query Match 3.9%; Score 84.4; DB 5; Length 2968;

XX Best Local Similarity 61.3%; Pred. No. 1.2e-12;

XX Matches 136; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

XX 1010 GAAGTGAACATGACAGGGGGAGCTGCAGAGAACTTCAATCTTCCAGAACCCGACTGAGGC 1069

XX 497 GAACCAAGCCTACAGATGAGAGGTGAATATGATTTGCTTCCAGAGCAAAATAGGTT 556

XX 1070 ATTGTGAAACATCATCTGATGCTGTACCAAGAGATTAAAGAACTGTGGGGGAG 1129

XX 557 AGTAAAGAAATGATGCTGAAGACACGACAGATGACAAAGATCTACGAGGAG 616

XX 1130 AAACCGGAGTTGTCCCAAAACAGAGATGGGCGAAGAAATATAGAGATTGACCCACA 1189

XX 617 AAATTACGCAATTCCTCCACACCGGAAATGACAGCAAAATATACGAGATTGACCCACA 676

XX 1190 CTGAAGATTTTCGAGGCGATCTTACTACCGGTAATGCTTA 1231

XX 677 CTCGAGACTTTAAGTACCATCTTGTAGTATGATATAGCCTA 718

XX RESULT 11

XX ABK15494

XX ID ABK15494 standard; cDNA; 3039 BP.

XX AC ABK15494;

XX 08-MAY-2002 (first entry)

XX Wheat starch branching enzyme IIb cDNA from clone wdk2c\_pk009.j17.

XX Wheat starch branching enzyme; starch synthesis; transgenic plant;

XX wdk2c\_pk009.j17; antibody; gene mapping; expressed sequence tag; EST;

XX gene; ss.

XX Triticum aestivum.

XX Key Location/Qualifiers

XX CDS 3.2570

XX /\*tag= a

XX /product= "starch branching enzyme IIb"

XX /partial

/note= "No start codon shown. The sequence from nucleotides 481-3039 is specifically claimed in claim 3 of the specification and is shown as Seq ID. 1"

XX US2002002713-A1.

XX 03-JAN-2002.

XX 23-FEB-2001; 2001US-00792127.

XX 01-MAR-2000; 2000US-0186098P.

XX (ALLE) ALLEN S M.

XX (BECK) BECKLES D M.

XX (BUTL) BUTLER K H.

XX (PEAR) PEARLSTEIN R W.

XX Allen SM, Beckles DM, Butler KH, Pearlstein RW,

XX WPI; 2002-178959/23.

XX P-PDB; AAU76219.

XX Novel isolated polypeptide having starch IIb enzyme activity, useful for

XX preparing antibodies to the proteins which are used to detect the

XX polypeptides in situ in cells or in vitro in cell extracts.

XX Claim 3; Page 17-18; 27pp; English.

XX This invention relates to the cDNA and protein sequences of a novel wheat

XX starch branching enzyme IIb enzyme. Starch branching enzymes are

XX responsible for the formation of alpha 1-6 linkages in amylopectin in the

XX starch synthesis pathway. The nucleotide sequence of the invention is

XX useful for producing a transgenic plant expressing the starch branching

XX enzyme. The protein sequence is useful for preparing antibodies against

XX starch branching enzyme IIb protein, which are useful for detecting the

XX proteins in situ in cells, or in vitro in cell extracts. The protein is

XX also useful for selecting an isolated polynucleotide that affects the

XX level of expression of a starch branching enzyme IIb protein or enzyme

XX activity in a plant cell. All or substantial portion of the nucleotide

XX sequence can be used as probe for genetic and physical mapping of the

XX information in a plant cell. All or substantial portion of the nucleotide

XX sequence can be used as markers for traits linked to those genes. This

XX information is useful in plant breeding in order to develop lines with

XX desired phenotypes. A polynucleotide fragment is useful for isolating

XX cDNAs and genes encoding homologous proteins from the same or other plant

XX species. They are also useful as DNA hybridisation probes or as

XX polymerase chain reaction (PCR) amplification primers. The fragments are

XX also useful for creating transgenic plants and may be useful as

XX restriction fragment length polymorphism markers. Nucleic acid probes

XX derived from the cDNA sequence may also be used for physical mapping or

XX for fluorescence in situ hybridisation (FISH) mapping. The present

XX sequence represents the wheat starch branching enzyme IIb cDNA from clone

XX wdk2c\_pk009.j17

XX Sequence 3039 BP; 836 A; 624 C; 783 G; 796 T; 0 U; 0 Other;

XX Query Match 3.9%; Score 84.4; DB 6; Length 3039;

XX Best Local Similarity 61.3%; Pred. No. 1.3e-12;

XX Matches 136; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

XX 1010 GAAGTGAACATGACAGGGGGAGCTGCAGAGAACTTCAATCTTCCAGAACCCGACTGAGGC 1069

XX 372 GAACCAAGCCTACAGATGAGAGGTGAATATGATTTGCTTCCAGAGCAAAATAGGTT 431

XX 1070 ATTGTGAAACATCATCTGATGCTGTACCAAGAGATTAAAGAACTGTGGGGGAG 1129

XX 432 AGTAAAGAAATGATGCTGAAGACACGACGAGTGAAGCAAAATATAGAGATTGACCCACA 491

XX 1130 AAACCGGAGTTGTCCCAAAACAGAGATGGGCGAAGAAATATAGAGATTGACCCACA 1189

XX 492 AAATTACGCAATTCCTCCACACCGGAAATGACAGCAAAATATAGAGATTGACCCACA 551

XX 1190 CTGAAGATTTTCGAGGCGATCTTACTACCGGTAATGCTTA 1231

Db 552 CTCGAGACTTTAAGTACCATCTTGATGATGATAGACCTTA 593

## RESULT 12

AAH78341 ID AAH78341 standard; DNA, 3962 BP.

AC AAH78341;

XX 26-NOV-2001 (first entry)

DE Partial sequence of a starch branching enzyme designated F2.

XX Wheat; starch branching enzyme; BE11b; SBE; transgenic plant;

KM starch biosynthetic pathway; amylopectin; F2; amylose; ss.

XX Aegilops tauschii.

XX WO200162934-A1.

XX 30-AUG-2001.

XX 21-FEB-2001; 2001WO-AU000175.

XX 21-FEB-2000; 2000AU-00005742.

XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.

PA (GOOD-) GOODMAN FIELDER LTD.

PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.

XX Morell M, Rahman S;

XX WPI; 2001-570635/64.

XX Nucleic acids encoding wheat starch branching enzyme 11b, useful for

PT altering the amylose and amylopectin content of cereal plants, e.g. wheat

PT and barley.

XX Claim 6; Fig 8; 103p; English.

XX The present sequence represents a partial genomic sequence of a wheat

XX starch branching enzyme of Aegilops tauschii, designated F2. A. tauschii

XX is likely to be the ancestral D genome donor of wheat. Probes isolated F2

XX were used to identify type II starch branching enzymes (SBEs) in wheat,

XX especially BE11b. The BE11b nucleic acids may be used to generically

XX transform cereal plants such as wheat or barley and for altering their

XX nutritional content by modulating the starch biosynthetic pathway to vary

XX levels of amylopectin and/or amylose produced in the plant

XX Sequence 3962 BP; 1091 A; 778 C; 809 G; 1284 T; 0 U; 0 Other;

XX Query Match 3.8%; Score 82.2; DB 5; Length 3962;

XX Best Local Similarity 61.4%; Pred. No. 6.2e-12;

XX Matches 132; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

XX 1010 GAAGTGAACATGACAGGGGGGACCTGACAGAGAACTTCAATCTTCAGAACCGACTCAGGGC 1069

XX 1156 GAAACAGGCTACAGATGAGGTGAAGATGATTTGGCTTCAGAGCAAAATCAGGTT 1215

XX 1070 ATTGTGAAACAATCACTGATGCTGTAAACCAAGAGCTTAAGAACTAGTGTGGGGGAG 1129

XX 1216 AGTGAAGAAATGATGCTGTAAGACAGACAGATGACAAAGATCATCTACAGAGGAG 1275

XX 1130 AAACCGCGAGTGTCCCAAAACAGAGATGGGCAAAAATATACGATGACCCACACA 1189

XX 1276 AAATTAAGCAATCTGCGACACCGGAAATGACAGCAAAATATACGATTGACCCACAG 1335

XX 1190 CTGAAGATTTTGGAGCCATCTTGACTACCGGTA 1224

XX 1336 CTCGAGACTTTAAGTACCATCTTGATGATGATAGACCTTA 1370

XX RESULT 13

AAH78343 ID AAH78343 standard; DNA, 8381 BP.

AC AAH78343;

XX 26-NOV-2001 (first entry)

DE Partial genomic sequence of wheat starch branching enzyme (BE11b).

XX Wheat; starch branching enzyme; BE11b; SBE; transgenic plant;

KM starch biosynthetic pathway; amylopectin; amylose; ss.

XX Triticum sp.

XX WO200162934-A1.

XX 30-AUG-2001.

XX 21-FEB-2001; 2001WO-AU000175.

XX 21-FEB-2000; 2000AU-00005742.

XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.

PA (GOOD-) GOODMAN FIELDER LTD.

PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.

XX Morell M, Rahman S;

XX WPI; 2001-570635/64.

XX Nucleic acids encoding wheat starch branching enzyme 11b, useful for

PT altering the amylose and amylopectin content of cereal plants, e.g. wheat

PT and barley.

XX Claim 6; Page 95-98; 103p; English.

XX The present sequence represents a partial genomic sequence of a wheat

XX starch branching enzyme, designated BE11b. BE11b is a type II starch

XX branching enzyme (SBE). The BE11b nucleic acids may be used to

XX genetically transform cereal plants such as wheat or barley and for

XX altering their nutritional content by modulating the starch biosynthetic

XX pathway to vary levels of amylopectin and/or amylose produced in the

XX plant

XX Sequence 8381 BP; 2134 A; 1788 C; 1829 G; 2608 T; 0 U; 22 Other;

XX Query Match 3.8%; Score 82.2; DB 5; Length 8381;

XX Best Local Similarity 61.4%; Pred. No. 9.5e-12;

XX Matches 132; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

XX 1010 GAAGTGAACATGACAGGGGGGACCTGACAGAGAACTTCAATCTTCAGAACCGACTCAGGGC 1069

XX 1616 GAAACAGGCTACAGATGAGGTGAAGATGATTTGGCTTCAGAGCAAAATCAGGTT 1675

XX 1070 ATTGTGAAACAATCACTGATGCTGTAAACCAAGAGCTTAAGAACTAGTGTGGGGGAG 1129

XX 1676 AGTGAAGAAATGATGCTGTAAGACAGACAGATGACAAAGATCATCTACAGAGGAG 1735

XX 1130 AAACCGCGAGTGTCCCAAAACAGAGATGGGCAAAAATATACGATGACCCACACA 1189

XX 1736 AAATTAAGCAATCTGCGACACCGGAAATGACAGCAAAATATACGATTGACCCACAG 1795

XX 1190 CTGAAGATTTTGGAGCCATCTTGACTACCGGTA 1224

XX 1796 CTCGAGACTTTAAGTACCATCTTGATGATGATAGACCTTA 1830

XX RESULT 14

XX AA073750 ID AA073750 standard; cDNA to mRNA; 2919 BP.

XX AA073750;

XX

DT 05-JUL-1995 (first entry)  
XX Rice starch branching enzyme.  
DE Starch branching enzyme; rice; starch content; ds.  
XX  
XX Oryza sativa.  
OS  
XX  
XX Key Location/Qualifiers  
FH 1.127  
FT 5/UTR /tag= a  
FT transit\_peptide 128..322  
FT /tag= b  
FT mat\_peptide 323..2606  
FT /tag= c  
FT /product= "branching\_enzyme"  
FT 2603..2919  
FT 3/UTR /tag= d  
XX  
XX JF06261767-A.  
XX  
XX 20-SEP-1994.  
XX  
XX 22-OCT-1993; 93JP-00265171.  
XX  
XX 29-OCT-1992; 92JP-00291719.  
XX  
XX (MITSU) GYOSAI SHOKUBUTSU BIO KENKYUSHO.  
XX WPI: 1994-337418/42.  
XX P-PSDB: AAR60811.  
DR  
XX New gene of branching enzyme of rice starch - useful for increasing  
PT starch yield of grain.  
XX  
XX Claim 1; Page 9-12; 13pp; Japanese.  
PS  
XX The rice starch branching enzyme is encoded by the cDNA sequence  
CC AA073750. The starch content of rice grains can be increased by  
CC increasing the expression of branching enzyme in rice plants  
CC  
XX Sequence 2919 BP; 755 A; 590 C; 800 G; 774 T; 0 U; 0 Other;  
SQ  
Query Match 3.7%; Score 79.4; DB 2; Length 2919;  
Best Local Similarity 63.2%; Pred. No. 3.2e-11;  
Matches 122; Conservative 0; Mismatches 71; Indels 0; Gaps 0;  
QY 1039 GAAACTTCAATCTTGAAGACGACCTCAGGCGATTGTGAAACAATCAGTGTGTAAC 1098  
DB 436 GAGAGTTGAGAGCTGAAGTTGAGATTGATGATCTGAGCAAGTGTGAAAGCGTGA 495  
QY 1099 CAAAGCATTAAGAGACTAGTCGTGGGGAGAAACCGCAGTTGTCCAAAACCAAGAG 1158  
DB 496 GAGAGTGTGTAAGATTAGCTGCTGAGAGAAACCAAGTTGTCCCAACCAAGAGAG 555  
QY 1159 TGGGCAAAATATACGAGATTGACCCCAACTGAAAGATTTTGGAGGCATTTGACTA 1218  
DB 556 TGGGCAAAAAATATTCAGATGAGATCTATGCTTAATGCTAATAGTACCATCTTGAATA 615  
QY 1219 CCGGTAATGCCCTA 1231  
DB 616 TCGATATAGCCTA 628  
RESULT 15  
ADCO7807  
ID ADC07807 standard; DNA; 2307 BP.  
XX  
XX ADC07807;  
AC  
XX 18-DEC-2003 (first entry)  
DT  
XX Rice DNA sequence Seq ID73 related to grain filling.  
DB

XX plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;  
XX carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;  
XX tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;  
XX wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;  
XX Gene; ds; plant.  
XX  
XX Oryza sativa.  
OS  
XX  
XX WO2003000905-A2.  
XX  
XX 03-JAN-2003.  
XX  
XX 21-JUN-2002; 2002MO-IB002450.  
XX  
XX 22-JUN-2001; 2001US-0300112P.  
XX 26-SEP-2001; 2001US-0325277P.  
XX 20-DEC-2001; 2001US-0342327P.  
XX  
XX (SYGN) SYNGENTA PARTICIPATIONS AG.  
XX  
XX Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;  
PI Glazebrook J, Katagiri F, Kreps J, Provart N, Riecke D;  
XX  
XX WPI: 2003-229341/22.  
XX P-PSDB; ADC07808.  
DR  
XX  
XX New plant genes encoding polypeptides having an activity involved in or  
PT associated with the synthesis, metabolism or degradation of carbohydrates  
PT in the plant grain useful in generating plants having improved  
PT nutritional properties.  
XX  
XX Claim 2; SEQ ID NO 73; 130pp; English.  
PS  
XX  
XX This invention, in the area of plant biotechnology, relates to novel  
CC polynucleotides comprising a nucleotide sequence encoding a protein which  
CC is involved in or associated with the synthesis, metabolism or  
CC degradation of carbohydrates in the plant grain and the expression of  
CC which is up-regulated during grain filling. The plant is selected from  
CC corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,  
CC sugarbeet, wheat, and rice. The invention may be useful for the  
CC improvement of protein, oil, starch, fibre and moisture content of the  
CC cereal grains. In addition, carbohydrate levels may be modified to a more  
CC desirable level using the present invention. The present sequence is a  
CC DNA sequence encoding a rice protein of the invention. Note: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/publishepct\_sequences.  
XX  
SQ Sequence 2307 BP; 608 A; 465 C; 620 G; 614 T; 0 U; 0 Other;  
Query Match 3.7%; Score 78.6; DB 5; Length 2307;  
Best Local Similarity 90.5%; Pred. No. 4.7e-11;  
Matches 95; Conservative 0; Mismatches 9; Indels 1; Gaps 1;  
QY 1618 AACGATACACCGAATCAAGAGATTCGTCGCTATTAAG-CCAACTGAAGGTGATT 1676  
DB 364 ACCGGAATACGATGATCAAGAGATTCGTCGCTATTAAG-CCAACTGAAGGTGATT 423  
QY 1677 GGAAGCATTTTCTCGTGTATGAAAAGCTTGAATTACCCGAG 1721  
DB 424 GGAATGATTTTCTCGTGTATGAAAAGCTTGAATTACCCGAG 468  
Search completed: April 10, 2004, 04:00:00  
Job time : 846.046 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

CM nucleic - nucleic search, using SW model

Run on: April 10, 2004, 03:15:35 ; Search time 152.665 Seconds  
(without alignments)  
7804.525 Million cell updates/sec

Title: US-09-508-377-10\_COPY\_1058\_3204  
Sequence: 2147  
1 cgcacgtccaccccccgc.....tgcagatactatgcacagag 2147

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/ECTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfillseq1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	243	11.3	2853	4 US-09-609-040-3	Sequence 3, Appl
2	90.8	4.2	2446	4 US-09-731-166-9	Sequence 9, Appl
3	68.8	3.2	7218	1 US-08-232-463-14	Sequence 14, Appl
4	61.6	2.9	2720	4 US-09-731-166-11	Sequence 11, Appl
5	58.4	2.7	2087	4 US-09-257-894-9	Sequence 9, Appl
6	58.4	2.7	2165	4 US-09-257-894-8	Sequence 8, Appl
7	58.4	2.7	2665	4 US-08-257-894-1	Sequence 1, Appl
8	58.4	2.7	2725	4 US-08-941-445A-14	Sequence 14, Appl
9	58.2	2.7	3074	3 US-09-087-877-1	Sequence 1, Appl
10	58.2	2.5	507	4 US-09-257-894-5	Sequence 5, Appl
11	53.8	2.1	7218	1 US-08-232-463-14	Sequence 14, Appl
12	43.4	2.0	832	4 US-09-621-876-2813	Sequence 2813, Ap
13	43.4	2.0	832	4 US-09-621-876-2813	Sequence 2813, Ap
14	42.2	2.0	279	4 US-09-113-294A-3795	Sequence 3795, Ap
15	41.2	1.9	364	4 US-09-621-876-17202	Sequence 17202, A
16	41.1	1.9	819	4 US-09-252-991A-7968	Sequence 7968, Ap
17	41.1	1.9	3657	4 US-09-252-991A-8298	Sequence 8298, Ap
18	41.1	1.9	3661	4 US-09-252-991A-8018	Sequence 8018, Ap
19	40.2	1.9	832	4 US-09-621-876-2813	Sequence 2813, Ap
20	40	1.9	1427	1 US-07-994-133-1	Sequence 1, Appl
21	40	1.9	1427	6 5196304-1	Patent No. 5196304
22	39.6	1.8	3001	4 US-09-539-333D-184	Sequence 184, App
23	38.4	1.8	1281	3 US-09-105-537-19	Sequence 19, Appl
24	38.4	1.8	13613	3 US-09-105-537-3	Sequence 3, Appl
25	38.4	1.8	38506	4 US-09-320-878-19	Sequence 19, Appl
26	38.4	1.8	38506	4 US-09-411-908-1	Sequence 1, Appl
27	38.4	1.8	38506	4 US-09-657-440-19	Sequence 19, Appl

28	37.6	1.8	330	4 US-09-313-294A-7061	Sequence 7061, Ap
29	37.6	1.8	395	4 US-09-894-844-45	Sequence 45, Appl
30	37.6	1.8	1600	4 US-09-434-288-10	Sequence 10, Appl
31	37.6	1.8	4252	2 US-08-475-844-4	Sequence 4, Appl
32	37.6	1.8	4252	5 PCT-US95-08429-4	Sequence 4, Appl
33	37.2	1.7	2830	1 US-07-882-292-1	Sequence 1, Appl
34	37.2	1.7	2830	2 US-08-331-644-1	Sequence 1, Appl
35	37.2	1.7	2830	5 PCT-US93-04102-1	Sequence 1, Appl
36	37.2	1.7	1664976	4 US-08-916-421B-1	Sequence 1, Appl
37	36.8	1.7	4403765	3 US-09-103-840A-2	Sequence 2, Appl
38	36.8	1.7	4411529	3 US-09-103-840A-2	Sequence 1, Appl
39	36.6	1.7	441	4 US-09-252-991A-16329	Sequence 16329, A
40	36.6	1.7	1029	4 US-09-252-991A-16157	Sequence 16157, A
41	36.6	1.7	1272	4 US-09-252-991A-16045	Sequence 16045, A
42	36.6	1.7	1296	4 US-08-894-844-47	Sequence 47, Appl
43	36.6	1.7	1980	4 US-09-252-991A-16555	Sequence 16555, A
44	36.6	1.7	2561	4 US-09-616-289-48	Sequence 48, Appl
45	36.6	1.7	12732	3 US-09-060-756-1	Sequence 1, Appl

## ALIGNMENTS

RESULT 1  
US-09-609-040-3  
Sequence 3, Application US/09609040  
Patent No. 6570066  
GENERAL INFORMATION:  
APPLICANT: Wilmittzer, et al.  
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING ENZYMES THAT ALTER THE CARBOHYDRATE  
TITLE OF INVENTION: CONCENTRATION AND COMPOSITION IN PLANTS  
FILE REFERENCE: 514413-3515.1  
CURRENT APPLICATION NUMBER: US/09/609,040  
PRIOR FILING DATE: 2000-06-30  
CURRENT FILING DATE: 1992-02-11  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 3  
LENGTH: 2853  
TYPE: DNA  
ORGANISM: Triticum aestivum  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (313)..(2499)  
OTHER INFORMATION: BRANCHING ENZYME  
US-09-609-040-3

Query Match	11.3%	Score 243;	DB 4;	Length 2853;
Best Local Similarity	98.0%	Pred. No. 1.8e-60;		
Matches 246;	Conservative	0;	Mismatches 5;	Indels 0;
			Gaps	0;
QY	978	AGATACCTGAAGATTCGAGGCAACGCGGAAGTGAACATGACAGGGGACTGCAG	1037	
DB	272	AGATACCTGAAGATTCGAGGCAACGCGGAAGTGAACATGACAGGGGACTGCAG	331	
QY	1038	AGAACTTCAATCTTGAGAACCGACTCAGGCGATTGTGAAACATCACTGATGGTGTAA	1097	
DB	332	AAAACTTCAATCTTGAGAACCGACTCAGGCGATTGTGAAACATCACTGATGGTGTAA	391	
QY	1098	CCAAAGGCTTAAGAACTAGTCGTGGGGGAGAAACCGGAGTGTCCCAAAACAGAG	1157	
DB	392	CCAAAGGCTTAAGAACTAGTCGTGGGGGAGAAACCGGAGTGTCCCAAAACAGAG	451	
QY	1158	ATGGGCAAAAATATACGAGATTGACCAACACTGAAAGATTTCGAGCCATCTTGACT	1217	
DB	452	ATGGGCAAAAATATACGAGATTGACCAACACTGAAAGATTTCGAGCCATCTTGACT	511	
QY	1218	ACCGGTAATGC 1228		
DB	512	ACCGGTAATGC 522		





FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (0)...(0)  
OTHER INFORMATION: SBE1B  
OTHER INFORMATION: Genbank Accession No. 6639126 AF072725  
NAME/KEY: CDS  
LOCATION: (101)...(2500)  
US-09-731-166-11

Query Match 2.9%; Score 61.6; DB 4; Length 2720;  
Best Local Similarity 76.0%; Pred. No. 1.9e-07;  
Matches 76; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1622 GATACAGCGAATACAGAGAAATTCGTCTATTGACCAACATGAAGGTGATTGGAAG 1681  
DB 513 GGACAGCCCTCTATAGAGAAATCCGTTCAACATTTGATGACATGAAGAGAGCTTGGAAG 572  
QY 1682 CATTTCTCGTGTATGAAAAGCTTGATTACCCGAG 1721  
DB 573 CCTTCTCCGTAATGAGAACTTGATTATCCAG 612

RESULT 5  
US-09-257-894-9  
Sequence 9, Application US/09257894  
Patent No. 6376749

GENERAL INFORMATION:  
APPLICANT: Broglie, Karen E.  
APPLICANT: Klein, Theodore M.  
APPLICANT: Hubbard, Natalie L.  
APPLICANT: Lightner, Jonathan E.  
TITLE OF INVENTION: No. 6376749e1 Starches via Modification of  
TITLE OF INVENTION: Expression of Starch Biosynthesis  
TITLE OF INVENTION: Enzyme Genes  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: E. I. du Pont de Nemours and Company  
STREET: 1007 Market Street  
CITY: Wilmington  
STATE: Delaware  
COUNTRY: USA  
ZIP: 19898  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Microsoft Windows 95  
SOFTWARE: Version 7.0A  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/257,894  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/091,052  
FILING DATE: JUNE 10, 1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Majarian, William R.  
REGISTRATION NUMBER: 41,173  
REFERENCE/DOCKET NUMBER: BB-1066-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 302-992-4926  
TELEFAX: 302-773-0164  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2087 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-257-894-9

Query Match 2.7%; Score 58.4; DB 4; Length 2087;  
Best Local Similarity 74.0%; Pred. No. 1.4e-06;  
Matches 74; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1622 GATACAGCGAATACAGAGAAATTCGTCTATTGACCAACATGAAGGTGATTGGAAG 1681  
DB 413 GGACAGCCCTCTATAGAGAAATCCGTTCAACATTTGATGACATGAAGAGAGCTTGGAAG 472  
QY 1682 CATTTCTCGTGTATGAAAAGCTTGATTACCCGAG 1721  
DB 473 CCTTCTCCGTAATGAGAACTTGATTATCCAG 512

RESULT 6  
US-09-257-894-8/c  
Sequence 8, Application US/09257894  
Patent No. 6376749

GENERAL INFORMATION:  
APPLICANT: Broglie, Karen E.  
APPLICANT: Klein, Theodore M.  
APPLICANT: Hubbard, Natalie L.  
APPLICANT: Lightner, Jonathan E.  
TITLE OF INVENTION: No. 6376749e1 Starches via Modification of  
TITLE OF INVENTION: Expression of Starch Biosynthesis  
TITLE OF INVENTION: Enzyme Genes  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: E. I. du Pont de Nemours and Company  
STREET: 1007 Market Street  
CITY: Wilmington  
STATE: Delaware  
COUNTRY: USA  
ZIP: 19898  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Microsoft Windows 95  
SOFTWARE: Version 7.0A  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/257,894  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/091,052  
FILING DATE: JUNE 10, 1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Majarian, William R.  
REGISTRATION NUMBER: 41,173  
REFERENCE/DOCKET NUMBER: BB-1066-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 302-992-4926  
TELEFAX: 302-773-0164  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2165 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-257-894-8

Query Match 2.7%; Score 58.4; DB 4; Length 2165;  
Best Local Similarity 74.0%; Pred. No. 1.4e-06;  
Matches 74; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1622 GATACAGCGAATACAGAGAAATTCGTCTATTGACCAACATGAAGGTGATTGGAAG 1681  
DB 1675 GGACAGCCCTCTATAGAGAAATCCGTTCAACATTTGATGACATGAAGAGAGCTTGGAAG 1616  
QY 1682 CATTTCTCGTGTATGAAAAGCTTGATTACCCGAG 1721  
DB 1615 CCTTCTCCGTAATGAGAACTTGATTATCCAG 1576

RESULT 7  
US-09-257-894-1

Sequence 1, Application US/09257894  
Patent No. 6376749  
GENERAL INFORMATION:  
APPLICANT: Broglie, Karen E.  
APPLICANT: Klein, Theodore M.  
APPLICANT: Hubbard, Natalie L.  
APPLICANT: Lightner, Jonathan E.  
TITLE OF INVENTION: No. 6376749el Starches via Modification of  
TITLE OF INVENTION: Expression of Starch Biosynthesis  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: E. I. du Pont de Nemours and Company  
STREET: 1007 Market Street  
CITY: Wilmington  
STATE: Delaware  
COUNTRY: USA  
ZIP: 19898  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Microsoft Windows 95  
SOFTWARE: Version 7.0A  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/257,894  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/091,052  
FILING DATE: JUNE 10, 1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Majarian, William R.  
REGISTRATION NUMBER: 41,173  
REFERENCE/DOCKET NUMBER: BB-1066-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 302-992-4926  
TELEFAX: 302-773-0164  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2665 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURES:  
NAME/KEY: CDS  
LOCATION: 79..2476  
US-09-257-894-1

Query Match 2.7%; Score 58.4; DB 4; Length 2665;  
Best Local Similarity 74.0%; Pred. No. 1.6e-06;  
Matches 74; Conservative 0; Mismatches 26; Indels 0; Gaps 0;  
DB 1622 GATACAGCAATACAGAGAAATTCGCTGCTATTGACCAACATGAAGGTGATTGGAAG 1661  
491 GGTACAGCCTCTATAGAGATCCGTTGACACATGTGATGAACATGAAGAGGCTTGAAG 550  
QY 1682 CATTTCTCGTGCTATGAAAAGCTTGATTTACCCGCGAG 1721  
DB 551 CCTTCCCGTAGTATGAGAACTTTGATTATGCGCAG 590

RESULT 9  
US-08-941-445A-14  
Sequence 14, Application US/08941445A  
Patent No. 6107060  
GENERAL INFORMATION:  
APPLICANT: Keeling, Peter  
APPLICANT: Guan, Hanning  
TITLE OF INVENTION: Starch Encapsulation  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.

STREET: 5370 Manhattan Circle  
CITY: Boulder  
STATE: CO  
COUNTRY: US  
ZIP: 80303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/941,445A  
FILING DATE: 30-SEP-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/026,855  
FILING DATE: 30-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Winner, Ellen P  
REGISTRATION NUMBER: 28,547  
REFERENCE/DOCKET NUMBER: 89-97  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 499-8080  
TELEFAX: (303) 499-8089  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2725 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: not relevant  
MOLECULE TYPE: mRNA  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Zea mays  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 91..264  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 265..2487  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 91..2490  
US-08-941-445A-14

Query Match 2.7%; Score 58.4; DB 3; Length 2725;  
Best Local Similarity 74.0%; Pred. No. 1.6e-06;  
Matches 74; Conservative 0; Mismatches 26; Indels 0; Gaps 0;  
DB 1622 GATACAGCAATACAGAGAAATTCGCTGCTATTGACCAACATGAAGGTGATTGGAAG 1661  
503 GGTACAGCCTCTATAGAGAAATCCGTTGACACATGTGATGAACATGAAGAGGCTTGAAG 562  
QY 1682 CATTTCTCGTGCTATGAAAAGCTTGATTTACCCGCGAG 1721  
DB 563 CCTTCCCGTAGTATGAGAACTTTGATTATGCGCAG 602

RESULT 9  
US-09-087-277-1  
Sequence 1, Application US/09087277B  
Patent No. 6169226  
GENERAL INFORMATION:  
APPLICANT: EK, Bo  
APPLICANT: KHOSWOODI, Jamshid  
APPLICANT: LARSSON, Clas-Tomas  
APPLICANT: LARSSON, Hakar  
APPLICANT: RASK, Lars  
TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO  
FILE REFERENCE: 003300-486  
CURRENT APPLICATION NUMBER: US/09/087,277B  
CURRENT FILING DATE: 1998-05-29  
EARLIER APPLICATION NUMBER: PCT/SE96/01558

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; EARLIER FILING DATE: 1996-11-28
; EARLIER APPLICATION NUMBER: SE 9504272-7
; EARLIER FILING DATE: 1995-11-29
; EARLIER APPLICATION NUMBER: SE 9601506-0
; EARLIER FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3074
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:beli gene
; OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
; OTHER INFORMATION: (potato)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (189)..(2825)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (189)..(332)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (333)..(2825)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (92)..(2156)
; OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are
; OTHER INFORMATION: n wherein n = A, C, G or T.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (285)..(287)
; OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu, Val
; OTHER INFORMATION: or Phe.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1404)..(1406)
; OTHER INFORMATION: Amino acid 358 is Xaa wherein Xaa = Thr.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1428)..(1430)
; OTHER INFORMATION: Amino acid 366 is Xaa wherein Xaa = Thr.
; NAME/KEY: misc_feature
; LOCATION: (1896)..(1898)
; OTHER INFORMATION: Amino acid 522 is Xaa wherein Xaa = Tyr, Ser, Cys
; OTHER INFORMATION: or Phe.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2154)..(2156)
; OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro.
; US-09-087-277-1
;
; Query Match
; Best Local Similarity 72.8%; DB 3; Length 3074;
; Matches 75; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
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; QY 1619 ACAGATACACGCAATACAAAGAAATTCGTCGTATGACCAACATGAAGTGGATTGG 1678
; DB 775 ACAGGATTCACAGTACAAAGAACTGAGGAGGCAATTGACAACTATGAGGTTGG 834
;
; QY 1679 AAGCATTTTCGTCGTATGAAAAGCTTGATTACCCGAG 1721
; DB 835 AAGCTTTTCGTCGTATGAAAAAATGGCTTCACTCGTAG 877
;
; RESULT 10
; US-09-658-499-1
; Sequence 1, Application US/09658499
; Patent No. 6469231
; GENERAL INFORMATION:
; APPLICANT: EK, Bo
; APPLICANT: KHOSNODI, Jamshid

```

```

; APPLICANT: LARSSON, Clas-Tomas
; APPLICANT: LARSSON, Hakan
; APPLICANT: RASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/09/658,499
; CURRENT FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 09/087,277
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: PCT/SE96/01558
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: SE 9504272-7
; PRIOR FILING DATE: 1995-11-29
; PRIOR APPLICATION NUMBER: SE 9601506-0
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3074
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:beli gene
; OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
; OTHER INFORMATION: (potato)
; NAME/KEY: CDS
; LOCATION: (189)..(2825)
; NAME/KEY: sig_peptide
; LOCATION: (189)..(332)
; NAME/KEY: mat_peptide
; LOCATION: (333)..(2825)
; NAME/KEY: misc_feature
; LOCATION: (92)..(2156)
; OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are
; OTHER INFORMATION: n wherein n = A, C, G or T.
; NAME/KEY: misc_feature
; LOCATION: (285)..(287)
; OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu, Val
; OTHER INFORMATION: or Phe.
; NAME/KEY: misc_feature
; LOCATION: (1404)..(1406)
; OTHER INFORMATION: Amino acid 358 is Xaa wherein Xaa = Leu or Phe.
; NAME/KEY: misc_feature
; LOCATION: (1428)..(1430)
; OTHER INFORMATION: Amino acid 366 is Xaa wherein Xaa = Thr.
; NAME/KEY: misc_feature
; LOCATION: (1896)..(1898)
; OTHER INFORMATION: Amino acid 522 is Xaa wherein Xaa = Tyr, Ser, Cys
; OTHER INFORMATION: or Phe.
; NAME/KEY: misc_feature
; LOCATION: (2154)..(2156)
; OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro.
; US-09-658-499-1
;
; Query Match
; Best Local Similarity 72.8%; DB 4; Length 3074;
; Matches 75; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
;
; QY 1619 ACAGATACAGCAATACAAAGAAATTCGTCGTATGACCAACATGAAGTGGATTGG 1678
; DB 775 ACAGGATTCACAGTACAAAGAACTGAGGAGGCAATTGACAACTATGAGGTTGG 834
;
; QY 1679 AAGCATTTTCGTCGTATGAAAAGCTTGATTACCCGAG 1721
; DB 835 AAGCTTTTCGTCGTATGAAAAAATGGCTTCACTCGTAG 877
;
; RESULT 11
; US-09-257-894-5/C
; Sequence 5, Application US/09257894
; Patent No. 6376749
; GENERAL INFORMATION:
; APPLICANT: Brogile, Karen E.

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APPLICANT: Klein, Theodore M.  
APPLICANT: Hubbard, Natalie L.  
APPLICANT: Lightner, Jonathan E.  
TITLE OF INVENTION: No. 6376749e1 Starches via Modification of  
TITLE OF INVENTION: Expression of Starch Biosynthesis  
TITLE OF INVENTION: Enzyme Genes  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: E. I. du Pont de Nemours and Company  
STREET: 1007 Market Street  
CITY: Wilmington  
STATE: Delaware  
COUNTRY: USA  
ZIP: 19898  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Microsoft Windows 95  
SOFTWARE: Version 7.0A  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/257,894  
CLASSIFICATION:  
FILING DATE:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 09/091,052  
FILING DATE: JUNE 10, 1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Majarian, William R.  
REGISTRATION NUMBER: 41,173  
REFERENCE/DOCKET NUMBER: BB-1066-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 302-992-4926  
TELEFAX: 302-773-0164  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 507 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-257-894-5

Query Match 2.5%; Score 53.8; DB 4; Length 507;  
Best Local Similarity 69.5%; Pred. No. 1.2e-05;  
Matches 73; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 1126 GGAGAAACCGGAGTGTCTCCAAAACCGAGATGGGCGAATAATACGAGATTGACCC 1185  
DB 112 GAAACGAGTTGAGTGTCTCCAAAACCGAGATGGGCGAATAATACGAGATTGACCC 53

QY 1186 AACACTGAAAGATTTCGAGACCATCTTGACTACCGGTATGCTT 1230  
DB 52 CATGTTGCAAGCTATAGTACATCTTGAGTATCGTACAGCTT 8

RESULT 12  
US-08-232-463-14/c  
Sequence 14, Application US/08232463  
Patent No. 5670367  
GENERAL INFORMATION:  
APPLICANT: DORNER, F.  
APPLICANT: SCHREIFLINGER, F.  
APPLICANT: FALKNER, F. G.  
TITLE OF INVENTION: RECOMBINANT FOMPOX VIRUS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,463  
FILING DATE:  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/07/935,313  
FILING DATE:  
APPLICATION NUMBER: EP 91 114 300.6  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/114 IMU  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-9300  
TELEFAX: (703) 683-4109  
TELEX: 895149  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7218 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: pTZ19pt-F15  
US-08-232-463-14

Query Match 2.1%; Score 45; DB 1; Length 7218;  
Best Local Similarity 2.6%; Pred. No. 0.024; Indels 0; Gaps 0;  
Matches 6; Conservative 145; Mismatches 80; Indels 0; Gaps 0;

QY 967 TTTCGTCTGTAGATACCTGAGATATCGAGAGCAACCGCGAGTGAACATGACAG 1026  
DB 1442 TTTCGTACRR 1383

QY 1027 GGGGACTGCAGAACTTCAATCTTCAGAACCGACTCAGGCACTTGGAACAATAC 1086  
DB 1382 RRR 1323

QY 1087 TGATGTGTAACCAAGAGTTAAGACTGCTGGGAGGAACCGAGTGTGCC 1146  
DB 1322 RRR 1263

QY 1147 AAAACGAGATGGCGAGAAATAATACGAGTTGACCAACTGAAAGA 1197  
DB 1262 RRR 1212

RESULT 13  
US-09-621-976-2813  
Sequence 2813, Application US/09621976  
Patent No. 6639063  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J. B.  
APPLICANT: Jobert, S.  
APPLICANT: Giordano, J. Y.  
TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
FILE REFERENCE: GENSET.054PR2  
CURRENT APPLICATION NUMBER: US/09/621,976  
CURRENT FILING DATE: 2000-07-21  
NUMBER OF SEQ ID NOS: 19335  
SOFTWARE: Patent.pm  
SEQ ID NO 2813  
LENGTH: 832  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 235..399





```
QY 121 CTGGCTGACTCAATCACTACGCGGGGATGCGAGCTTCCGCGTGTCCGGCGGACCTCTCG 180
Db 1278 CTGGCTGACTCAATCACTACGCGGGGATGCGAGCTTCCGCGTGTCCGGCGGACCTCTCG 1237
QY 181 GTGTGGCGCGGCGCGCGCTCGGAGTGGCGCGGCGCGCTCGGAGCGGAGGCGCGGCGG 240
Db 1238 GTGTGGCGCGGCGCGCGCTCGGAGTGGCGCGGCGCGCTCGGAGCGGAGGCGCGGCGG 1297
QY 241 ACTTCCGCTGCTGCTCCAGAGAAAGAAAGAACTCTCTCTGTAAGCGCTGCTCTCTGAT 300
Db 1298 ACTTCCGCTGCTGCTCCAGAGAAAGAAAGAACTCTCTCTGTAAGCGCTGCTCTCTGAT 1357
QY 301 CTCCCGCGCTGAGCTTGTGCTCCCTCTCTCTCTGCGCGCGCATGCGCTGTCTGAT 360
Db 1358 CTCCCGCGCTGAGCTTGTGCTCCCTCTCTCTCTGCGCGCGCATGCGCTGTCTGAT 1417
QY 361 GCTGTTCCTCCCAATTCATCTCCATGATGAGAGAGTACTGATTTAGCGCATCGCGCTTC 420
Db 1418 GCTGTTCCTCCCAATTCATCTCCATGATGAGAGAGTACTGATTTAGCGCATCGCGCTTC 1477
QY 421 CTGAACCTGTATTTTTCCTCCCGCGGAGAAATGCTGTAGTGCACCCAGGCGCTGTGT 480
Db 1478 CTGAACCTGTATTTTTCCTCCCGCGGAGAAATGCTGTAGTGCACCCAGGCGCTGTGT 1537
QY 481 ACCAGCGCTTGTGATCATCTCTGCTTTCATCTGTGATATATTTTCTCATTTCTTTCTTC 540
Db 1538 ACCAGCGCTTGTGATCATCTCTGCTTTCATCTGTGATATATTTTCTCATTTCTTTCTTC 1597
QY 541 CTGTCTCTGTGTAACTGCAAGTGTGGCGTTTTCCTCACTATGTAGTCACTCTGCTGAT 600
Db 1598 CTGTCTCTGTGTAACTGCAAGTGTGGCGTTTTCCTCACTATGTAGTCACTCTGCTGAT 1657
QY 601 TTGAGCGCGCGCTCTGAGCGCGCGCGCTCTGAGAGAGAGTCTGTGCTGACGCGG 660
Db 1658 TTGAGCGCGCGCTCTGAGCGCGCGCGCTCTGAGAGAGAGTCTGTGCTGACGCGG 1717
QY 661 AGAG-GAGGACTTGGCAAGTCCGCGGCACTGAGAAATTAAGTAAACACACCTGCTGC 719
Db 1718 AGAGGAGGACTTGGCAAGTCCGCGGCACTGAGAAATTAAGTAAACACACCTGCTGC 1777
QY 720 CGGTAAATCTTCATACAACTGCTTATTCATTAACAAATGCGGATGAGAAACCAACGGA 779
Db 1778 CGGTAAATCTTCATACAACTGCTTATTCATTAACAAATGCGGATGAGAAACCAACGGA 1837
QY 780 TGGCTGAGTTTCGAGCTTCTTATTCAGCAATGTGAGTACTGCTGCTGTCTTCAAT 839
Db 1838 TGGCTGAGTTTCGAGCTTCTTATTCAGCAATGTGAGTACTGCTGCTGTCTTCAAT 1897
QY 840 TTGTAGCTTGGCGCGCGCTGCTGCTGCGCGCACTGAGAAATTAAGTAAATGAT 899
Db 1898 TTGTAGCTTGGCGCGCGCTGCTGCTGCGCGCACTGAGAAATTAAGTAAATGAT 1957
QY 900 TCTAGCAAGAACTTCACAACTATATGACCGTTTGGGTTTCTGCTGCTGCTGAT 959
Db 1958 TCTAGCAAGAACTTCACAACTATATGACCGTTTGGGTTTCTGCTGCTGCTGAT 2017
QY 960 TGTATTTTTCGCTGTGATGATCTGAAAGATTAAGAGAGAAACGCGGAGAGTAA 1019
Db 2018 TGTATTTTTCGCTGTGATGATCTGAAAGATTAAGAGAGAAACGCGGAGAGTAA 2077
QY 1020 TGAACGCGGAGTGGCAAGAACTTCATCTTCAAGACCGACTCAGGCGATTTGAGAA 1079
Db 2078 TGAACGCGGAGTGGCAAGAACTTCATCTTCAAGACCGACTCAGGCGATTTGAGAA 2137
QY 1080 CAATCACTGATGCTGTAAACCAAGAGTTAAAGAACTGTGCTGCGGAGAAACCGGAG 1139
Db 2138 CAATCACTGATGCTGTAAACCAAGAGTTAAAGAACTGTGCTGCGGAGAAACCGGAG 2197
QY 1140 TTGTCCCAAAACAGAGATGAGGAGAAATATAGAGATTGACCAACATGAAAGATT 1199
Db 2198 TTGTCCCAAAACAGAGATGAGGAGAAATATAGAGATTGACCAACATGAAAGATT 2257
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QY 1200 TTGGAGCCATCTTACTACCGGTAATGCTTACCCGCTGCTTCCGCTCATTTGATTA 1259
Db 2258 TTGGAGCCATCTTACTACCGGTAATGCTTACCCGCTGCTTCCGCTCATTTGATTA 2317
QY 1260 GGTCTTTTCATGATGCAAAATTTGGGGAACATCAAAAGACAAAGACTAGGACCACT 1319
Db 2318 GGTCTTTTCATGATGCAAAATTTGGGGAACATCAAAAGACAAAGACTAGGACCACT 2377
QY 1320 TCATACAGATCCCTTCGATGCTGAGATPAGTGGGAAAGTAAATGATTAATGATGCT 1379
Db 2378 TCATACAGATCCCTTCGATGCTGAGATPAGTGGGAAAGTAAATGATTAATGATGCT 2437
QY 1380 ACAATTTGCTCAAAATTTGCAATACGAAATACGTCTCCGATCATTAATTAAGAGTGG 1439
Db 2438 ACAATTTGCTCAAAATTTGCAATACGAAATACGTCTCCGATCATTAATTAAGAGTGG 2497
QY 1440 CAACCTGATGAAATATGATGAGTGGATTAAGATTTTACTTGTGCTAATTCCTCAACAA 1499
Db 2498 CAACCTGATGAAATATGATGAGTGGATTAAGATTTTACTTGTGCTAATTCCTCAACAA 2557
QY 1500 ATTCTAGGCGGGAATCTACCAATGAGGAAACTAGTTCTTATCTTGTGCGCTTTT 1559
Db 2558 ATTCTAGGCGGGAATCTACCAATGAGGAAACTAGTTCTTATCTTGTGCGCTTTT 2617
QY 1560 GTTTTGGGAAAAACATGCTTAAATTTGAAATGATTTTGGTATACCTGCTGATTCAA 1619
Db 2618 GTTTTGGGAAAAACATGCTTAAATTTGAAATGATTTTGGTATACCTGCTGATTCAA 2677
QY 1620 CAGATACGCGAATACAAAGAAATTCGCTGCTATTAAGCAACATGAAAGTGGATGGA 1679
Db 2678 CAGATACGCGAATACAAAGAAATTCGCTGCTATTAAGCAACATGAAAGTGGATGGA 2737
QY 1680 AGCATTTTCTGTGATTAAGAAAGCTTGAATTAACCGGAGTAAATTTAAAGCTTAT 1739
Db 2738 AGCATTTTCTGTGATTAAGAAAGCTTGAATTAACCGGAGTAAATTTAAAGCTTAT 2797
QY 1740 TATATGAAAGCGCTCCGCTAGCTGATTAATGATTAATTAAGAAATTTAAATTCCTG 1799
Db 2798 TATATGAAAGCGCTCCGCTAGCTGATTAATGATTAATTAAGAAATTTAAATTCCTG 2857
QY 1800 TTTTCCCTCTCTTTTTCAGAGCTGAGGATGCTAATTTGATTAATGATTAAGAA 1859
Db 2858 TTTTCCCTCTCTTTTTCAGAGCTGAGGATGCTAATTTGATTAATGATTAAGAA 2917
QY 1860 ATTATATCTGTTTTCCTTATTTTTCAGTGTGAAAGTATCACTTAACGAGATGG 1919
Db 2918 ATTATATCTGTTTTCCTTATTTTTCAGTGTGAAAGTATCACTTAACGAGATGG 2977
QY 1920 CTCCTGAGCGCAATGATATGCTTAAAGTCTTAAAGACAGACACTTCAATTAAT 1979
Db 2978 CTCCTGAGCGCAATGATATGCTTAAAGTCTTAAAGACAGACACTTCAATTAAT 3037
QY 1980 GTTAATGTCATATTCACCACTAGTCTTGAATTAAGTAAATTAAGTAACT 2039
Db 3038 GTTAATGTCATATTCACCACTAGTCTTGAATTAAGTAAATTAAGTAACT 3097
QY 2040 GACCACTTACTAATTAATTAATGATGCTTGAACCTTCAAGCTGAGAGATTAAG 2099
Db 3098 GACCACTTACTAATTAATTAATGATGCTTGAACCTTCAAGCTGAGAGATTAAG 3157
QY 2100 TAGTGACTTCAACAAATTTGAATCCAAATGAGATTAATTAAGCAAG 2147
Db 3158 TAGTGACTTCAACAAATTTGAATCCAAATGAGATTAATTAAGCAAG 3205
```

RESULT 2  
US-10-434-893A-1  
; Sequence 1, Application US/10434893A  
; Publication No. US2004060083A1  
; GENERAL INFORMATION:  
; APPLICANT: Ahmed Regina  
; APPLICANT: Matthew Kennedy Morell  
; APPLICANT: Sadequr Rahman



```

?
?
? TITLE OF INVENTION: Barley with altered branching enzyme activity and starch and
?
? TITLE OF INVENTION: containing products with an increased amylose content
? FILE REFERENCE: 69425
?
? CURRENT APPLICATION NUMBER: US/10/434,893A
?
? CURRENT FILING DATE: 2003-05-09
?
? NUMBER OF SEQ ID NOS: 11
?
? SOFTWARE: PatentIn version 2.1
?
? SEQ ID NO 1
?
? LENGTH: 2554
?
? TYPE: DNA
?
? ORGANISM: Hordeum vulgare
?
? FEATURE:
?
? OTHER INFORMATION: SSBELIA CDNA
?
US-10-434-893A-1

```

OTHER INFORMATION: n is a, c, g or t  
FEATURE:  
OTHER INFORMATION: partial SSBELIB gene  
US-10-434-893A-4

Query Match 3.8%; Score 82.2; DB 12; Length 6550;  
Best Local Similarity 61.4%; Pred. No. 2e-12;  
Matches 132; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 1010 GAAGTGAATGACAGAGGGGGAATGACAGAACTTCAATCTTCAGAGACCGACTCAGGGC 1069  
DB 1616 GAAACAGGCTACAGATGAGGTGAAGATGATTTGCTTCAGAGACAAATCAGGTT 1675  
QY 1070 ATTGTGAAACAATCACTGATGTTGTTAACCAGATTAAGAACTAGTCTGAGGAG 1129  
DB 1676 AGTGAAGAAATGATGATGTTGAAGACAGACGAGATGACAAAGATCATCTACAGAGGAG 1735  
QY 1130 AAACCCGAGTTGTCCCAAAACAGAGATGGCGAGAAATATACGATTTGACCCACA 1189  
DB 1736 AATATGCACTTGTGCACACCGGAAATGACAGCAATATACGATTTGACCCACA 1795  
QY 1190 CTGAAGAATTTTGGAGCCATCTTGACTACCGTA 1224  
DB 1796 CTCGAGACTTTAAGTACCATCTTGATTCGTA 1830

RESULT 6  
US-09-792-127-1  
Sequence 1, Application US/09792127  
Patent No. US20020002713A1  
GENERAL INFORMATION:  
APPLICANT: Allen, Steve  
APPLICANT: Beckles, Diane M.  
APPLICANT: Butler, Karla  
APPLICANT: Pearlstein, Rich  
TITLE OF INVENTION: Starch Branching Enzyme IIB  
FILE REFERENCE: B1439 US NA  
CURRENT APPLICATION NUMBER: US/09/792,127  
CURRENT FILING DATE: 2001-02-23  
PRIOR APPLICATION NUMBER: 60/166098  
PRIOR FILING DATE: 2000-03-01  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: Microsoft Office 97  
SEQ ID NO: 1  
LENGTH: 2559  
TYPE: DNA  
ORGANISM: Triticum aestivum  
US-09-792-127-1

Query Match 3.0%; Score 64.2; DB 9; Length 2559;  
Best Local Similarity 74.3%; Pred. No. 2.2e-07;  
Matches 81; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1123 GGGGAGAAACCGCGAGTTGTCCAAAACAGAGATGGGCGAGAAATATACGAGTTGA 1182  
DB 5 GAGGAGAAATTAAGCATCTCTCCACACCGGAAATGACAGCAATATACGAGTTGA 64  
QY 1183 CCCAACACTGAAGATTTTGGAGCATTTTGACTTACCGGTATGCTTA 1231  
DB 65 CCCAACGCTCCGAGACTTTAAGTACCATCTTGATGATATAGCTTA 113

RESULT 7  
US-10-424-599-130848  
Sequence 130848, Application US/10424599  
Publication No. US20040031072A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa Thomas J  
APPLICANT: Kovalic David K  
APPLICANT: Zhou Yihua  
APPLICANT: Cao Yongwei  
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)B  
CURRENT APPLICATION NUMBER: US/10/424,599  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 285684  
SEQ ID NO 130848  
LENGTH: 470  
TYPE: DNA  
ORGANISM: Glycine max  
OTHER INFORMATION: Clone ID: PAT\_MBT3847\_89163C.1  
US-10-424-599-130848

Query Match 3.0%; Score 63.6; DB 12; Length 470;  
Best Local Similarity 59.3%; Pred. No. 9.2e-08;  
Matches 108; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 1548 TGTGGCTTTTGTGTTGGGAAACACATTCCTAATTCGATGATTTGGGTATACCT 1607  
DB 154 TTTTGCACTTTTGATACCTACTATCTGTAATTTATACGTAAATTTTAAATGCTA 213  
QY 1608 CGGTGATTTCAACAGATACGCGAATACAGAGAAATGCTGCTGCTATGACCAAGTGA 1667  
DB 214 TTTTAAATCACAGTTATGACAAATACAAAGATTGCGTTATGAATGACAGCTGA 273  
QY 1668 AGGTGATTTGAGAGATTTTCTCGGTATGAAAAGCTTGATTTACCCGAGTAAAT 1727  
DB 274 AGCGGCTCGATTAATTTTCACTGCTGTTATGAATAATTTGCTTCCAGCGAGTATTA 333  
QY 1728 TT 1729  
DB 334 TT 335

RESULT 8  
US-09-938-842A-337  
Sequence 337, Application US/09938842A  
Patent No. US20020160378A1  
GENERAL INFORMATION:  
APPLICANT: Harper, Jeff  
APPLICANT: Kreps, Joel  
APPLICANT: Wang, Xun  
APPLICANT: Zhu, Tong  
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
TITLE OF INVENTION: SAME, AND METHODS OF USE  
FILE REFERENCE: SRIPI300-3  
CURRENT APPLICATION NUMBER: US/09/938,842A  
CURRENT FILING DATE: 2001-08-24  
PRIOR APPLICATION NUMBER: US 60/227,866  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: US 60/264,647  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/300,111  
PRIOR FILING DATE: 2001-06-22  
NUMBER OF SEQ ID NOS: 5379  
SEQ ID NO 337  
LENGTH: 2577  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
US-09-938-842A-337

Query Match 2.8%; Score 59.8; DB 9; Length 2577;  
Best Local Similarity 73.8%; Pred. No. 4.5e-06;  
Matches 76; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 1619 ACAGATACAGCGATACAGAGATTCGTCTGCTATTTGACCAACATGAAAGTGATTCG 1678  
DB 527 ACGGATATGGGCACTACAGAAACCTGCTGAAGAAATGAAAGATGAAGGTGTTGG 586  
QY 1679 AAGCATTTTCTGCTGTTATGAAAAGCTTGATTTACCCGAG 1721  
DB 587 AGGATTTTCTGCTGTTATGAAAATTTGCTTCACTGGAAG 629

## RESULT 9

US-09-938-842A-337  
Sequence 337, Application US/09938842A  
Publication No. US20040009476A9  
GENERAL INFORMATION:  
APPLICANT: Harper, Jeff  
APPLICANT: Kreps, Joel  
APPLICANT: Wang, Xun  
APPLICANT: Zhu, Tong  
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
TITLE OF INVENTION: SAME AND METHODS OF USE  
FILE REFERENCE: SRIPI300-3 US/09/938,842A  
CURRENT FILING DATE: 2001-08-24  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: US 60/227,866  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/264,647  
PRIOR FILING DATE: 2001-06-22  
PRIOR APPLICATION NUMBER: US 60/300,111  
NUMBER OF SEQ ID NOS: 5379  
SEQ ID NO 337  
LENGTH: 2577  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
US-09-938-842A-337

Query Match 2.8%; Score 59.8; DB 11; Length 2577;  
Best Local Similarity 73.8%; Pred. No. 4.5e-06;

Matches 76; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 1619 ACAGATACGCGAATCAAGAGATTGCTGCTATTTGACCAACATGAAGTGGATTGG 1678  
DB 527 ACCGATATGGGAGTACAGAAACTGCGTGAAGAAATGACAGAAATGAAGTGGTGG 586

QY 1679 AAGCATTTCTCGTGGTTATGAAGAGTTTACCCGCG 1721  
DB 587 AGCGATTTCTCGTGGTTATGAAGATTTGGCTTACCTGAG 629

## RESULT 10

US-10-056-454A-18  
Sequence 18, Application US/10056454A  
Publication No. US20030166919A1

## GENERAL INFORMATION:

APPLICANT: National Starch and Chemical Investment Holding Corporation  
TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: National Starch and Chemical Investment Holding Corporation  
STREET: 1000 Unidema Blvd.  
CITY: Newcastle  
STATE: Delaware  
COUNTRY: United States of America  
ZIP: 19720

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/056,454A  
FILING DATE: 25-Jun-2002  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3231 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-10-056-454A-18  
SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Query Match 2.8%; Score 59.8; DB 14; Length 3231;

Best Local Similarity 73.8%; Pred. No. 5.3e-06;  
Matches 76; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 1619 ACAGATACGCGAATCAAGAGATTGCTGCTATTTGACCAACATGAAGTGGATTGG 1678  
DB 814 ACAGTATTCACAGTACAGAAATGAGGAGGCAATTGACAGTATGAGGTGGTTGG 873

QY 1679 AAGCATTTCTCGTGGTTATGAAGAGTTTACCCGCG 1721  
DB 874 AAGCTTTCTCGTGGTTATGAAGAAATTTGGCTTACCTGAG 916

## RESULT 11

US-10-424-599-130849  
Sequence 130849, Application US/10424599  
Publication No. US20040031072A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa Thomas J  
APPLICANT: Kovalic David K  
APPLICANT: Zhou Yihua  
APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
FILE REFERENCE: 38-21(53223)B  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 285684  
SEQ ID NO 130849  
LENGTH: 5164  
TYPE: DNA  
ORGANISM: Glycine max

OTHER INFORMATION: Clone ID: PAT\_MRT3847\_89164C.1  
US-10-424-599-130849

Query Match 2.7%; Score 58.8; DB 12; Length 5164;  
Best Local Similarity 73.5%; Pred. No. 1.5e-05;  
Matches 75; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 1620 CAGATACGCGAATCAAGAGATTGCTGCTATTTGACCAACATGAAGTGGATTGGA 1679  
DB 927 CCGTATGAGACATCAAGAGATTGCTGCTATTTGACCAACATGAAGTGGATTGGA 986

QY 1680 AAGCATTTCTCGTGGTTATGAAGAGTTTACCCGCG 1721  
DB 987 TAGATTTCTCGTGGTTATGAAGAAATTTGGCTTACATGCGAG 1028

## RESULT 12

US-10-397-954A-1  
Sequence 1, Application US/10397954A  
Publication No. US2003022120A1

## GENERAL INFORMATION:

APPLICANT: Pearlstein, Richard W.  
APPLICANT: Broglie, Karen E.  
APPLICANT: Hines, Christopher F.  
TITLE OF INVENTION: Maize Starch Containing Elevated Amounts of Actual Amylose  
FILE REFERENCE: BB1510 US NA  
CURRENT FILING DATE: 2003-03-26  
PRIOR FILING DATE: 2002-03-27  
PRIOR APPLICATION NUMBER: 60/368,387  
PRIOR FILING DATE: 2002-03-27  
PRIOR APPLICATION NUMBER: 60/381,534  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: Microsoft Word 97  
SEQ ID NO 1  
LENGTH: 2443  
TYPE: DNA  
ORGANISM: Artificial Sequence

FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)..(2443)

OTHER INFORMATION: SBEII modified region  
US-10-397-954A-1

Query Match 2.7%; Score 58.4; DB 15; Length 2443;  
Best Local Similarity 74.0%; Pred. No. 1.1e-05;  
Matches 74; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1622 GATACAGCGAATACAGAGAAATTCGTCTATTGACCAATGAGAGGTGGATTGAG 1681  
DB 418 GGTACAGCCCTTATAGAGAAATCCGTTGACATTTGATGAAATGAGAGAGGCTTGAG 477

QY 1682 CATTTTCTCGTGTATGAAAAGCTTGATTACCCGAG 1721  
DB 478 CCTTCTCCGTAGTATGAGAAAGTTGATTATATGCGAG 517

RESULT 13  
US-10-397-954A-1/C

Sequence 1, Application US/10397954A  
Publication No. US20030221220A1

GENERAL INFORMATION:

APPLICANT: Pearlstein, Richard W.

APPLICANT: Bregille, Karen E.

APPLICANT: Hines, Christopher F.

TITLE OF INVENTION: Maize Starch Containing Elevated Amounts of Actual Amylose

FILE REFERENCE: B1510 US NA

CURRENT APPLICATION NUMBER: US/10/397,954A

CURRENT FILING DATE: 2003-03-26

PRIOR APPLICATION NUMBER: 60/368,387

PRIOR FILING DATE: 2002-03-27

PRIOR APPLICATION NUMBER: 60/381,534

PRIOR FILING DATE: 2002-05-16

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Microsoft Word 97

SEQ ID NO 1

LENGTH: 2443

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

NAME/KEY: misc feature

LOCATION: (1)-(2443)

OTHER INFORMATION: SBEII modified region

US-10-397-954A-1

Query Match 2.7%; Score 58.4; DB 15; Length 2443;  
Best Local Similarity 74.0%; Pred. No. 1.1e-05;  
Matches 74; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1622 GATACAGCGAATACAGAGAAATTCGTCTATTGACCAATGAGAGGTGGATTGAG 1681  
DB 2024 GGTACAGCCCTTATAGAGAAATCCGTTGACATTTGATGAAATGAGAGAGGCTTGAG 1965

QY 1682 CATTTTCTCGTGTATGAAAAGCTTGATTACCCGAG 1721  
DB 1964 CCTTCTCCGTAGTATGAGAAAGTTGATTATATGCGAG 1925

RESULT 14

US-10-056-454A-17

Sequence 17, Application US/10056454A

Publication No. US20030166919A1

GENERAL INFORMATION:

APPLICANT: National Starch and Chemical Investment Holding Corporation

TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESS: National Starch and Chemical Investment Holding Corporation

STREET: 1000 UniGema Blvd.

CITY: Newcasttle

STATE: Delaware

COUNTRY: United States of America

ZIP: 19720

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/056,454A  
FILING DATE: 25-Jun-2002  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2529 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
US-10-056-454A-17

Query Match 2.7%; Score 58.2; DB 14; Length 2529;  
Best Local Similarity 72.8%; Pred. No. 1.3e-05;  
Matches 75; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1619 ACAGATACAGCGAATACAGAGAAATTCGTCTATTGACCAATGAGAGGTGGATTG 1678  
DB 501 ACAGATACAGCGAATACAGAGAAATTCGTCTATTGACCAATGAGAGGTGGATTG 560

QY 1679 AAGCATTTTCTCGTGTATGAAAAGCTTGATTACCCGAG 1721  
DB 561 AAGCATTTTCTCGTGTATGAAAAGCTTGATTACCCGAG 603

RESULT 15

US-10-056-454A-16

Sequence 16, Application US/10056454A

Publication No. US20030166919A1

GENERAL INFORMATION:

APPLICANT: National Starch and Chemical Investment Holding Corporation

TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESS: National Starch and Chemical Investment Holding Corporation

STREET: 1000 UniGema Blvd.

CITY: Newcasttle

STATE: Delaware

COUNTRY: United States of America

ZIP: 19720

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/056,454A

FILING DATE: 25-Jun-2002

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 2576 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-10-056-454A-16

Query Match 2.7%; Score 58.2; DB 14; Length 2576;  
Best Local Similarity 72.8%; Pred. No. 1.3e-05;  
Matches 75; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1619 ACAGATACAGCGAATACAGAGAAATTCGTCTATTGACCAATGAGAGGTGGATTG 1678  
DB 508 ACAGATACAGCGAATACAGAGAAATTCGTCTATTGACCAATGAGAGGTGGATTG 567

QY 1679 AAGCATTTTCTCGTGTATGAAAAGCTTGATTACCCGAG 1721  
DB 568 AAGCATTTTCTCGTGTATGAAAAGCTTGATTACCCGAG 610

Mon Apr 12 10:24:23 2004

us-09-508-377-10\_copy\_1058\_3204.rmpb

Page 7

Search completed: April 10, 2004, 20:07:30  
Job time : 766.289 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 10, 2004, 03:15:20 ; Search time 5665.27 Seconds  
(without alignments)  
11317.033 Million cell updates/sec

Title: US-09-508-377-10\_COPY\_1058\_3204

Perfect score: 2147  
Sequence: 1 CGCAGCTCCACCCCGCC.....TGCAGATACATGACAGAG 2147

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 segs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estmu:\*  
5: em\_estrov:\*  
6: em\_estrpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_esthum:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_huv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rpd:\*  
26: em\_gss\_rpg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	238.2	11.1	623	14	CA726861 weif.pko
2	235	10.9	483	13	BQ239365 TAE05031H
3	235	10.9	604	14	CD925132 G750.11SP
4	223.8	10.4	577	13	CA025454 H252D11r

Result No.	Score	Query Match	Length	DB ID	Description
5	183.2	8.5	412	13	CA029212
6	150.2	7.0	297	14	CA500698
7	136.6	6.4	219	12	BM441043
8	135.8	6.3	831	14	CB629365
9	131.4	6.1	1066	29	CG421032
10	117.8	5.5	189	13	BQ754975
11	100.2	4.7	342	10	BE590829
12	98.6	4.6	517	13	BE590829
13	98.6	4.6	556	9	AV913706
14	98.6	4.6	556	13	BQ240653
15	92.6	4.3	129	12	BM368073
16	90.8	4.2	2766	11	AY109521
17	84.2	3.9	752	14	CD423046
18	81.2	3.8	830	28	CC421433
19	81.2	3.8	841	29	CC607582
20	81.2	3.8	846	29	CC607572
21	81.2	3.8	949	29	CC631299
22	81.2	3.8	949	29	CG340947
23	80.8	3.8	806	28	AQ864199
24	80.2	3.7	381	28	BZ407662
25	80.2	3.7	524	12	BG901327
26	80.2	3.7	561	13	BU099131
27	80.2	3.7	574	29	CG308966
28	80.2	3.7	718	28	BZ538816
29	80.2	3.7	720	28	BZ732892
30	80.2	3.7	788	28	BZ644713
31	80.2	3.7	825	28	BZ732883
32	80.2	3.7	844	29	CC730667
33	80.2	3.7	912	29	CG308966
34	80.2	3.7	919	29	CG300534
35	80.2	3.7	928	29	CG199431
36	80.2	3.7	984	29	CG172191
37	77.6	3.6	410	29	CG732805
38	75.4	3.5	947	29	CG308838
39	73.8	3.4	625	28	BZ775600
40	70.8	3.3	357	28	BZ644719
41	69	3.2	847	29	CG300518
42	67.6	3.1	480	9	AJ476662
43	67.6	3.1	480	9	AJ476662
44	67.4	3.1	693	28	BZ407668
45	64.8	3.0	388	12	BM443964

## ALIGNMENTS

RESULT 1  
CA726861  
LOCUS  
DEFINITION  
wdeif.pk002.g8 wdeif Triticum aestivum cDNA clone wdeif.pk002.g8 5'  
end, mRNA sequence.  
ACCESSION  
CA726861  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Triticum aestivum (bread wheat)  
Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Triticum.  
REFERENCE  
1 (bases 1 to 623)  
Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hairey,C., Yuan,Z.,  
Miao,G., Caraher,N. and Hanafey,M.K.  
JOURNAL  
Unpublished (2002)  
CONTACT  
Contact: Scott V. Tingey  
Crop Genetics  
E. I. Dupont de Nemours and Company  
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA  
Tel: 302-631-2602  
Fax: 302-631-2607  
Email: Scott.V.Tingey@usa.dupont.com  
Seq primer: M13.  
Location/Qualifiers

## FEATURES

source

1..623  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4565"  
/clone="wdef.pk002.98"  
/tissue\_type="endosperm"  
/lab\_host="DH103"  
/clone\_lib="wdef"  
/note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2: XhoI; Wheat (Triticum aestivum, Hi line) developing endosperm 2-7 DPA"

ORIGIN

Query Match 11.1%; Score 238.2; DB 14; Length 623;  
Best Local Similarity 96.8%; Pred. No. 4e-40;  
Matches 243; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 978 AGATACCTGAAGATATCGAGAGCAACCGCGGAAGTGAACATGACAGGGGGGACTGCAG 1037  
DB 283 AGATACCTGAAGATATCGAGAGCAACCGCGTGAAGTGAACATGACAGGGGGGACTGCAG 342  
QY 1038 AGAACTTCAATCTTCAGAACCGACTCAGGCACTTGGAACAATCACTGATGTGTA 1097  
DB 343 AAAAACTTGAATCTTCAGAACCGACTCAGGCACTTGGAACAATCACTGATGTGTA 402  
QY 1098 CCAAGAGATTAAAGAACTAGTCTGCGGGGAGAAACCGCGAGTTTCCCAAAACAGAG 1157  
DB 403 CCAAGAGATTAAAGAACTAGTCTGCGGGGAGAAACCGCGAGTTTCCCAAAACAGAG 462  
QY 1158 ATGGGCGAATAATATACGAGATTGACCCACACCTGAAGAATTTCCGAGGCACTTGACT 1217  
DB 463 ATGGGCGAATAATATACGAGATTGACCCACACCTGAAGAATTTCCGAGGCACTTGACT 522  
QY 1218 ACCGTAATGC 1228  
DB 523 ACCGTAATGC 533

RESULT 2  
BQ239365 483 bp mRNA linear EST 03-MAY-2002  
LOCUS TaE05031H05R TaE05 Triticum aestivum cDNA clone TaE05031H05R, mRNA  
DEFINITION sequence.  
ACCESSION BQ239365  
VERSION BQ239365.1 GI:20435241  
KEYWORDS EST.  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum  
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticaceae; Triticum.  
1 (bases 1 to 483)  
Cloutier,S.  
Wheat functional genome - Glenlea developing seeds cDNA libraries unpublished (2002)  
Contact: Dr. Sylvie Cloutier  
Cereal Research Centre, Agriculture and Agri-food Canada  
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9  
Tel: (204) 983-2340  
Fax: (204) 983-4604  
Email: scloutier@agr.gc.ca  
was cloned directionally, not all sequences generated with reverse primer were from the 5' end (same with forward primer and 3' end).  
Average insert size is >2.0 kb  
Plate: 031 row: H column: 05  
Seq primer: M13 Reverse.  
Location/Qualifiers  
1..483  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/cultivar="Glenlea"  
/db\_xref="taxon:4565"  
/clone="TaE05031H05R"

FEATURES  
source

source

/tissue\_type="developing seeds"  
/dev\_stage="5 days after anthesis"  
/lab\_host="E. coli DH103"  
/clone\_lib="TaE05"  
/note="Vector: pSPORT-P (Invitrogen Technologies); Site 1: NotI; Site 2: MluI; mRNA obtained from wheat seeds of cultivar Glenlea 5 days post-anthesis"

ORIGIN

Query Match 10.9%; Score 235; DB 13; Length 483;  
Best Local Similarity 96.0%; Pred. No. 1.8e-39;  
Matches 241; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 978 AGATACCTGAAGATATCGAGAGCAACCGCGGAAGTGAACATGACAGGGGGGACTGCAG 1037  
DB 109 AGATACCTGAAGATATCGAGAGCAACCGCGTGAAGTGAACATGACAGGGGGGACTGCAG 168  
QY 1038 AGAACTTCAATCTTCAGAACCGACTCAGGCACTTGGAACAATCACTGATGTGTA 1097  
DB 169 AAAAACTTGAATCTTCAGAACCGACTCAGGCACTTGGAACAATCACTGATGTGTA 228  
QY 1098 CCAAGAGATTAAAGAACTAGTCTGCGGGGAGAAACCGCGAGTTTCCCAAAACAGAG 1157  
DB 229 CCAAGAGATTAAAGAACTAGTCTGCGGGGAGAAACCGCGAGTTTCCCAAAACAGAG 288  
QY 1158 ATGGGCGAATAATATACGAGATTGACCCACACCTGAAGAATTTCCGAGGCACTTGACT 1217  
DB 289 ATGGGCGAATAATATACGAGATTGACCCACACCTGAAGAATTTCCGAGGCACTTGACT 348  
QY 1218 ACCGTAATGC 1228  
DB 349 ACCGTAATGC 359

RESULT 3  
CD925132 604 bp mRNA linear EST 15-JUL-2003  
LOCUS G750.115P1F010709 G750 Triticum aestivum cDNA clone G750115P11,  
DEFINITION mRNA sequence.  
ACCESSION CD925132  
VERSION CD925132.1 GI:36772896  
KEYWORDS EST.  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum  
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticaceae; Triticum.  
1 (bases 1 to 604)  
Genoplante.  
Genoplante, a major partnership french program in plant genomics unpublished (2002)  
Contact: Genoplante  
Genoplante  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french plant genome programme 'genoplante' (<http://www.genoplante.com> and <http://genoplante-info.info.genogen.fr>).  
Location/Qualifiers  
1..604  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/cultivar="reclat1"  
/db\_xref="taxon:4565"  
/clone="G750115P11"  
/tissue\_type="grain (750 degrees per day after pollination)"  
/clone\_lib="G750"

ORIGIN

Query Match 10.9%; Score 235; DB 14; Length 604;  
Best Local Similarity 96.0%; Pred. No. 1.9e-39;



Query Match	10.4%	Score 223.8	Pid. 13	Length 577
Best Local Similarity	93.28%	Mismatches 17	Gaps 0	
Matches 234	Conservative			
QY	978 AGATACCTGAAGATATCGAGGACCAACGGCGGAGTGAACATGACAGGGGGGACTGACG	1037		
Db	307 AGGTACTGAAGATATCGAGGAGGAATGGCGGAGTAACATGACAGGGGGGCTCGAG	366		
QY	1038 AGAACTTCATCTTTCGAAACCGACTCAGGGCATTTGGGAAACAATCATCTGATGGCTTAA	1097		
Db	367 AAAAATTGATCTTTCGAAACCGACTCTCAGGGGATTTGGGAAACATCATCTGATGGCTTAA	426		
QY	1098 CCAAAGAGTTAAGAACTAGTGTGGGGGAGAAACCGCAGTTGTCCCAAAACAGAG	1157		
Db	427 CCAAAGAGTTAAGAACTAGTGTGGGGGAGAAACCGCAGTTGTCCCAAAACAGAG	486		
QY	1158 ATGGGCGAATAATATACGAGATTGACCCAACTGTAAGATTTTGGAGGCATCTTGAAT	1217		
Db	487 ATGGGCGAATAATAATACGAGATTGACCCAACTGTAAGATTTTGGAGGCATCTTGAAT	546		
QY	1218 ACCGTAATATGC 1228			

DB	54 / ACCGATACGC 55 /
RESULT 5	
CA029212	
ADMS	
CA029212	
412 bp	
mrna	
linear	
EST 24-OCT-2002	

LOCUS	CHROMOSOME	DEFINITION
602222	1	HZ64118r HZ Hordeum vulgare

5 - PRIME, mRNA sequence:  
ACCESSION CA029212

VERSION	CA029212.1	GI:24307176
KEYWORDS	EST.	

SOURCE	Hordeum vulgare subsp.
ORGANISM	Hordeum vulgare subsp.

Eukaryota; Viridiplantae

Spermatophyta; Magnoliaceae; Poideae; Triticeae; H

REFERENCE	1 (bases 1 to 412)
AUTHORS	Radchuk, V., Zhang, H., W

TITLE	ESTS from development
Barley ESTS from development	
Published (2002)	

DOORWAY	CONTACTS (2002)
COMMENT	Contact: Stein Nils

MOLECULAR MARKERS GROUP  
Institute of Plant Genes

Corrensstr. 3, 06466, C  
Tel: 039482-5522

Fax: 039482-5595  
Email: [stein@ink-caters.com](mailto:stein@ink-caters.com)

Insert Length: 412

Plate: 64 ROW: 1 COL: 1  
Seq primer: M13rev.

FEATURES	Location/Qual:
source	1. .412

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/organism="Homo sapiens"
/mol_type="mRNA"
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/cultivar="bar

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/sub_species=
/db_xref="GABI

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/db_xref="taxo
/clone="HZ6411

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/tissue_type='
/dev stage="0:
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/lab_host="XLI
```

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clone_id="h
/note="Vector
```

CDNA) ; Site\_2  
DAP(days after

caused by the  
present, as we

excise the inn

cloning system used Blue/white selection for recombinants  
is not 100% reliable. Average insert size is 900 bp"

## ORIGIN

Query Match 8.5%; Score 183.2; DB 13; Length 412;  
Best Local Similarity 93.6%; Pred. No. 2e-28; Indels 0; Gaps 0;  
Matches 191; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1025 GGAGGAGCTGCAGAGAACTTCATCTTCAGAACCGACTGAGGGCTATTGGAAACATC 1084  
DB 1 GGAGGGGCTGCAGAGAACTTCATCTTCAGAACCGACTGAGGGCTATTGGAAACATC 60  
QY 1085 ACTGATGTGTAACTCAAGAGATTAGGAACTAGTGTGGGGAGAAACCGGATTGTC 1144  
DB 61 ACTGATGTGTAACTCAAGAGATTAGGAACTAGTGTGGGGAGAAACCGGATTGTC 120  
QY 1145 CCAAAACAGAGATGGGCGAGAAATATAGAGATTGACCCACACTGAAAGATTTCGG 1204  
DB 121 CCAAAACAGAGATGGGCGAGAAATATAGAGATTGACCCACACTGAAAGATTTCGG 180  
QY 1205 AGCCATCTTACTACCGGTATGCG 1228  
DB 181 AGCCATCTTACTACCGGTATGCG 204

RESULT 6 297 bp mRNA linear EST 14-NOV-2002  
CA500698  
LOCUS WHE4023\_D10.H19PT wheat meiotic anther cDNA library Triticum  
DEFINITION aestivum cDNA clone WHE4023\_D10.H19, mRNA sequence.  
ACCESSION CA500698  
VERSION CA500698.1 GI:24991658  
KEYWORDS EST.  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Triticum.  
1 (bases 1 to 297)  
Anderson, O.D., Chao, S., Crossman, C., Langridge, P., Lazo, G.R.,  
Pham, J., Rausch, C.J., Sutton, T., Woo, J. and Wilson, C.  
The structure and function of the expressed portion of the wheat  
genomes - Meiotic anther cDNA library  
Unpublished (2002)  
Contact: Olin Anderson  
US Department of Agriculture, Agriculture Research Service, Pacific  
West Area, Western Regional Research Center  
800 Buchanan Street, Albany, CA 94710, USA  
Tel: 5105595773  
Fax: 5105595818  
Email: oanderson@pw.usda.gov  
Sequences have been trimmed to remove vector sequence and low  
quality sequence with phred score less than 20  
Seq primer: 17 primer.  
Location/Qualifiers

FEATURES  
source 1..297  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/cultivar="Chinese Spring"  
/db\_xref="taxon:4565"  
/clone="WHE4023\_D10.H19"  
/tissue\_type="Anther"  
/dev\_stage="Meiotic stages pre-meiosis-metaphase I"  
/lab\_host="E. coli DH10B"  
/clone\_lib="Wheat meiotic anther cDNA library"  
/note="Vector: pSPORT1, Site 1: SalI; Site 2: NotI; Plants  
were grown in a glasshouse. Anther meiotic stage was  
determined by removing anthers from individual primary  
florets. One anther was sacrificed for microscopic  
staging, and if determined to be between (and including)  
meiotic stages pre-meiosis and metaphase I, the remaining  
two anthers were collected and pooled for library  
construction. The tissue, total RNA, and poly(A) RNA were

## ORIGIN

Query Match 7.0%; Score 150.2; DB 14; Length 297;  
Best Local Similarity 85.6%; Pred. No. 2.1e-21; Indels 0; Gaps 0;  
Matches 167; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1 CGCCAGCTTCACACCCCGGACACGTTGCTCCCTTCATCGCTTCAATTATA 60  
DB 3 CGCCAGCTTCACACCCCGGACACGTTGCTCCCTTCATCGCTTCAATTATA 62  
QY 61 TCTCCATCACTGGGTTCCGCGCTGCATTTCGCGCGCGGTTGAGTACATCTGGCGCA 120  
DB 63 TCTCCATCACTGGGTTCCGCGCTGCATTTCGCGCGCGGTTGAGTACATCTGGCGCA 122  
QY 121 CTGCTGACTCATATCTACGCGGGGATGCGGACGTTCCGCGCGGACCTTCG 180  
DB 123 CTGACCGACTCACTCGCTGCGCGGGGATGCGCGCTTCGCGATTCCCGCTTCGCGCG 182  
QY 181 GTGTGGCGGCGGCGG 195  
DB 183 GTGTGGCGGCGGCGG 197

RESULT 7 219 bp mRNA linear EST 23-JUL-2002  
BM441043  
LOCUS EBed02\_SQ002\_E01.R endosperm, 8 DPA, no treatment, cv Optic, Ebed02  
DEFINITION Hordeum vulgare subsp. vulgare cDNA clone EBed02\_SQ002\_E01.5', mRNA  
sequence.  
ACCESSION BM441043  
VERSION BM441043.2 GI:21932253  
KEYWORDS EST.  
SOURCE Hordeum vulgare subsp. vulgare  
ORGANISM Hordeum vulgare subsp. vulgare  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Hordeum.  
1 (bases 1 to 219)  
Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudge, S., Cardie, L.,  
Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R.  
Development of Barley Transcriptome Resources  
Unpublished (2001)  
On Feb 1, 2002 this sequence version replaced gi:18471818.  
Contact: Waugh, R., Marshall, D.F.  
Genome Dynamics/Computational Biology  
Scottish Crop Research Institute  
Invergowrie, Dundee, DD2 5DA, Scotland, UK  
Tel: 00 44 1382 562731  
Fax: 00 44 1382 562426  
Email: eestec@scri.scri.ac.uk  
All sequence has a phred quality score of 20 or over  
Seq primer: M13 reverse.  
Location/Qualifiers

FEATURES  
source 1..219  
/organism="Hordeum vulgare subsp. vulgare"  
/mol\_type="mRNA"  
/cultivar="Optic"  
/sub\_species="Vulgare"  
/db\_xref="taxon:112509"  
/clone="EBed02\_SQ002\_E01"  
/tissue\_type="endosperm"  
/dev\_stage="8 DPA"  
/lab\_host="DH10B"  
/clone\_lib="endosperm, 8 DPA, no treatment, cv Optic,  
EBed02"  
/note="Vector: pSPORT1, Site 1: Sal I, Site 2: Not I;  
Non-normalised library, directionally cloned into pSPORT1.

prepared, cDNA synthesised, and directionally ligated into  
pSPORT1 by Tim Sutton in the P Langridge Lab at the  
Department of Plant Science, University of Adelaide, Waite  
Campus, Australia. Average insert size 1.5Kb. Plasmid DNA  
preparations and DNA sequencing were performed in the OD  
Anderson lab (all other authors)."

Derived from endosperm tissue dissected from developing  
grains (8 days post anthesis) in glasshouse grown barley  
plants. Developed as part of the barley transcriptome  
resources of BSRc/SEBRAD funded cereal IGF (Investigating  
resources of BSRc/SEBRAD funded cereal IGF (Investigating  
Gene function) project."

## ORIGIN

Query Match 6.4%; Score 136.6; DB 12; Length 219;  
Best Local Similarity 88.2%; Pred. No. 1.6e-18;  
Matches 172; Conservative 0; Mismatches 19; Indels 4; Gaps 2;

QY 90 TCGCCGCGCGGTTGAGTGAATCTGGGCGACTGCTGAATCAATACGCGGG-GAT 148  
DB 9 TGGGCGCGGTTGAGTGAATCTGGGCGACTGCTGAATCAATACGCGGGAGAT 68  
QY 149 GCGGACGTTCCGGGTGTCCGGGCGGCACTCTCGGTGGGCGGCGGCGGCGGAG---T 205  
DB 69 GCGGACGTTCCGGGTGTCCGGGCGGCACTCTCGGTGGGCGGCGGCGGCGGAGGCT 128  
QY 206 GCGGCGGCGGCGGCTCGAGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 265  
DB 129 GCGGCGGCGGCGGCTCGAGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 188  
QY 266 GAAGGACTCTCTCG 280  
DB 189 GAAGGACTCTCTCG 203

RESULT 8  
LOCUS CB629365 831 bp mRNA linear EST 08-APR-2003  
DEFINITION OS11B05120.f OS11B Oryza sativa (indica cultivar-group) cDNA  
clone OS11B05120 5', mRNA sequence.

ACCESSION CB629365  
VERSION CB629365.1 GI:29624354  
SOURCE EST.  
ORGANISM Oryza sativa (indica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 831)  
Jantasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E.,  
Kudrna, D., Dean, R., Soderlund, C., Wang, R. and Wang, G.

Large-scale identification of ESTs involved in the interaction  
between rice and Magnaporthe oryzae  
Unpublished (2003)

JOURNAL COMMENT  
Contact: Rod Wing  
Arizona Genomics Institute  
University of Arizona  
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ  
85721-0088, USA

FEATURES  
source  
1. 831  
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/mol\_type="mRNA"  
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/clone="OS11B05120"  
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/clone\_id="OS11B"  
/note="Vector: pBlueScript II KS +; Site 1: EcoRI; Site 2:  
XhoI; 24 hrs after inoculation with Rice Blast (P06-6-3)"

## ORIGIN

Query Match 6.3%; Score 135.8; DB 14; Length 831;  
Best Local Similarity 76.3%; Pred. No. 2.9e-18;  
Matches 167; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 1006 GGGGGAATGTAACATGACAGGGGAGTGGACAGAGAACTTCATCTTCAGAACCACTCA 1065  
DB 90 GGGAGAGCAAGCACTTAAGGTGTGGCTGAGAGCAAACTTGATCTTCAGAACTATCA 149  
QY 1066 GGGCATGTGGAACAATCACTGATGTGTATCAACCAAGAGTTAAGAACTAGTGGG 1125  
DB 150 AGACATTGAGAAATATGACTGAGGGGTGATCAAAATGCTGATGAACCAACTGTGA 209  
QY 1126 GGAGAAACCGGAGTGTGCCAAACCGAGAGATGGGCAAGAAATATGAGATGACCC 1185  
DB 210 GGATTAACCAAGATATCCACCAACGAGAGATGGGCAAGATATGACCAATGACCC 269  
QY 1186 AACCTGAAGATTTTGGAGCACTTGAATACCGTA 1224  
DB 270 AATCTGAAGATTTTGGAGCACTTGAATACCGTA 308

RESULT 9  
CG421022/c 1006 bp DNA linear GSS 22-SEP-2003  
LOCUS ZMMBc0034G11f ZMMBc (EcoRI) Zea mays subsp. mays genomic clone  
DEFINITION ZMMBc0034G11 5', genomic survey sequence.

ACCESSION CG421022  
VERSION CG421022.1 GI:34565867  
SOURCE GSS.  
KEYWORDS Zea mays subsp. mays (maize)  
Ze mays subsp. mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD  
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 1006)  
Bharti, A.K., Young, S., Kavchok, S., Keizer, G., Bronzino, A.C.,  
Zohovetz, V., Fu, G., Yu, Y., Wing, R. and Messing, J.

Sequencing of the maize genome at PGR (2003c)  
Unpublished (2003)  
Contact: Bharti, A.K.

JOURNAL COMMENT  
Dr. Joachim Messing's lab  
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers  
University  
190 Frelinghuysen Road, Piscataway, NJ 08854, USA

FEATURES  
source  
1. 1006  
/organism="Zea mays subsp. mays"  
/mol\_type="genomic DNA"  
/cultivar="B73"  
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/lab\_host="E. coli DH10B"  
/clone\_id="ZMMBc (EcoRI)"  
/note="Vector: pTARBC2.1; Site 1: EcoRI; Site 2: EcoRI"

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Query Match 6.1%; Score 131.4; DB 29; Length 1006;  
Best Local Similarity 60.1%; Pred. No. 2.6e-17;  
Matches 331; Conservative 0; Mismatches 176; Indels 44; Gaps 5;

QY 1597 TGGGTAACTCGGTGATTCACAGATACAGGAATACAGGAATTCGTCGCTATT 1656  
DB 782 TTGGTTGCTTTTGGATTCACAGATACAGGAATACAGGAATTCGTCGCTATT 723

QY	1657	GACCAACATGAAGGTGATTTGGAAAGCAATTTCTCGTGGTATGAAAAGCTTGATTAAC	1716
Db	722	GATCAACATGAAGGTGATTTGGATGCAATTTTCACGCGGTTACGAAAAGCTTGATTTACT	663
QY	1717	CGCAGTAAATTTTAAAGCTTTATTTATTTATGAAAGCGCTCCAGTCTAATTTGCATATCT	1776
Db	662	CGCAGGTAAATTTGTAAGCAATATGACATATG-----TTCTTTTAAATTAATCANGCATCT	609
QY	1777	TATAAGAAAATTTATTAATTCCTGTTTCCTCTCTTTTTCACGTGTGAAGTATCGT	1836
Db	608	TATAGCAAAATACGATTAC--AGTTTCCCCCTCTCTTTTCCAGCGCTGAAGGTATC--	554
QY	1837	CTAATTCGATATCTTATTAAGAAATTTATTTCTGTTTTCGCCATTTTCCAGTGTGCA	1896
Db	553	-----ACTTACGAGAAATGGGCTCTGTGAGCAATAGTATGTTCTTAAAGTTCCAT	505
QY	1897	AGGTATCACTTACCGAGATGGGCTCCCTGGAGCGCATGTATGTTCTTTTAAAGTTCCCT	1956
Db	504	GGCGATCACCTTTTAAACATGAT-----AGTGTCAATATTAACATGTTTAACTCTGTG	451
QY	1957	AACGAGACACCTTCCAAATTTATTTGTTAATGTCATATTTACCAACTTACCTTACTGCACT	2016
Db	450	CGCAATACGACACAGATAGTTTACACGAATATACGATTTCTCTCAAAAGAAATATAGTTTA	391
QY	2017	TACAAATTAGCTTACTGATATACTGACACCGTTACTATTAATTTATAGATGTGGCTTTTGAC	2076
Db	390	T-----CTTCCTGATCAACTCATTAATTAACATTTAAGAAAGGGTTCTTAAT	347
QY	2077	CCTGTTACGTCGTGAGCATAGTAGTGAGCATTTCAACATTTGAATCCAAATGCAGATAC	2136
Db	346	CTTACTGAGTCGTGAGCAATTAAGAAAGTACITTCACAACTGGAACCCAAATGCTGATGC	287
QY	2137	TATGACCGAG 2147	
Db	286	TATGGCCAGG 276	

RESULT 10  
B0754975  
LOCUS  
DEFINITION  
B0754975 189 bp mRNA linear EST 26-JUL-2002  
EBed02\_SQ003\_F18.R endosperm, 8 DPA, no treatment, cv Optic, EBed02c  
Hordium vulgare subsp. vulgare cDNA clone EBed02\_SQ003\_F18 5', mRNA  
sequence.  
B0754975  
B0754975.1 GI:21963447  
EST.  
Hordium vulgare subsp. vulgare  
Hordium vulgare subsp. vulgare  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Pooidae; Triticeae; Hordeum.  
1 (bases 1 to 189)  
Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardie, L.,  
Ramsey, L., Machray, G., Marshall, D. F. M. and Waugh, R.  
Development of Barley Transcriptome Resources  
Unpublished (2001)  
Contact: Waugh R., Marshall DF  
Genome Dynamics/Computational Biology  
Scottish Crop Research Institute  
Invergowrie, Dundee, DD2 5DA, Scotland, UK  
Tel: 00 44 1382 562731  
Fax: 00 44 1382 562426  
Email: estescrt.scri.ac.uk.

```

FEATURES
source
    location/Qualifiers
    1..189
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    /sub_species="vulgare"
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    /dev_stage="8 DPA"

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Ebed02"
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Non-normalised library, directionally cloned into pSPORT1.
Derived from endospERM tissue dissected from developing
grains (8 days post anthesis) in glasshouse grown barley
plants. Developed as part of the barley transcriptome
resources of BBSRC/SERAD funded cereal IGF (Investigating
Gene Function) project."

```

Query Match	5.5%	Score 117.8	DB 13	Length 189
Best Local Similarity	87.9%	Pred. 1.6e-14		
Matches 152	Conservative	0	Mismatches 17	Indels 4
			Gaps	2
Qy	112	TCCTGGCGCACTGGCTGACTCATCTCAACGCGG-GATGGCGACGTTGCGCGTGTCCGGC	170	
Db	1	TCCTGGCGACGCACTCCGCTCGCTGCTGCGCGGAGATGGGAGGTTGCGCGTGTCCGGC	60	
Qy	171	GCGACTCTCGGTGTGGGGCGGGCCGGGCTGGAG--TGCGCGCGCGCGCTCGGACGG	227	
Db	61	GCGACCTCTGGTGTGGCGGGCGCGCGGAGAGCGCTGCCGCATCCGCGCTCGGAGCGG	120	
Qy	228	AGGGCGGGCGGCACTGCGCTCGCTGCTCTCAAGAAAGAACTCTCTCG	280	
Db	121	AGGGCGGGCGGCACTGCGCTCGCTGCTCTCAAGAAAGAACTCTCTCG	173	

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RESULT 11
LOCUS BE590829
DEFINITION BE590829 342 bp mRNA linear EST 18-AUG-2000
aestivum CDNA clone WHE0855_F05_K09, mRNA sequence.
ACCESSION BE590829
VERSION BE590829.1 GI:3845902
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 342)
Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D.,
Han,P.S., Hsia,C.C., Kang,Y.Y., Lazo,G.R., Miller,R., Rauech,C.J.,
Seaton,C.L. and Tong,Y.C.
The structure and function of the expressed portion of the wheat
genomes - 20-45 DAP spike cDNA library
Unpublished (2000)
JOURNAL COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@w.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stragene, SK primer.
FEATURES
Location/Qualifiers
1..342

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/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Chinese Spring"
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/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
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/notes="Vector: Lambda Uni-ZAP XR, excised phageid;
Site_1: EORI; Site_2: XhoI; Plants were grown in the
greenhouse. Spikes at 20 DAP and seeds at 30 to 45 DAP

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we were harvested, total RNA and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give Bluescript phagemids in the T7 Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

## ORIGIN

Query Match 4.7%; Score 100.2; DB 10; Length 342;  
Best Local Similarity 97.1%; Pred. No. 1e-10; 3; Indels 0; Gaps 0;  
Matches 102; Conservative 0; Mismatches 3;

QY 1617 CACAGATACAGCGAATACAGAGAAATTCGTCGTATTTGACCAACATGAAGTGATT 1676  
17 CTACCGATACAGGAATACAGAGAAATTCGTCGTATTTGACCAACATGAAGTGATT 76  
QY 1677 GGAAGCATTTTCTCGTGTATGAAAAGCTTGATTTACCCGCAG 1721  
77 GGAAGCATTTTCTCGTGTATGAAAAGCTTGATTTACCCGCAG 121

RESULT 12 BU996927 517 bp mRNA linear EST 23-OCT-2002  
LOCUS H106F01r HI Hordeum vulgare subsp. vulgare cDNA clone H106F01  
DEFINITION 5-PRIME, mRNA sequence.

ACCESSION BU996927  
VERSION BU996927.1 GI:24273910  
KEYWORDS EST.  
SOURCE Hordeum vulgare subsp. vulgare  
ORGANISM Hordeum vulgare subsp. vulgare  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Hordeum.

REFERENCE 1 (bases 1 to 517)  
AUTHORS Zhang, H., Meschke, W., Michalek, W., Stein, N. and Gruner, A.  
TITLE EST sequencing and analysis in barley (2002)  
JOURNAL Unpublished (2002)  
COMMENT Contact: Stein Nils  
Molecular Markers Group, Department Genbank  
Institute of Plant Genetics and Crop Plant Research (IPK)  
Corrensstr. 3, 06466, Gatersleben, Germany  
Tel: 039482-5522  
Fax: 039482-5595  
Email: stein@ipk-gatersleben.de  
Insert Length: 517 Std Error: 0.00  
Plate: 6 Row: F Column: 1  
Seq primer: M13rev.

## FEATURES

source 1..517  
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/clone\_lib="HI"  
/note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of cDNA); Site 2: XhoI (3'-end of cDNA); Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinants is not 100% reliable."

ORIGIN 4.6%; Score 98.6; DB 13; Length 517;  
Query Match

Best Local Similarity 96.2%; Pred. No. 2.3e-10;  
Matches 101; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1617 CACAGATACAGCGAATACAGAGAAATTCGTCGTATTTGACCAACATGAAGTGATT 1676  
29 CTACCGATACAGGAATACAGAGAAATTCGTCGTATTTGACCAACATGAAGTGATT 88  
QY 1677 GGAAGCATTTTCTCGTGTATGAAAAGCTTGATTTACCCGCAG 1721  
89 GGAAGCATTTTCTCGTGTATGAAAAGCTTGATTTACCCGCAG 133

RESULT 13 AV913706 556 bp mRNA linear EST 18-JAN-2002  
LOCUS AV913706 K. Sato unpublished cDNA library, cv. Haruna Nijo  
DEFINITION germination shoots Hordeum vulgare subsp. vulgare cDNA clone  
bag823a09 5', mRNA sequence.

ACCESSION AV913706  
VERSION AV913706.1 GI:18209483  
KEYWORDS EST.  
SOURCE Hordeum vulgare subsp. vulgare  
ORGANISM Hordeum vulgare subsp. vulgare  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Hordeum.

REFERENCE 1 (bases 1 to 556)  
AUTHORS Sato, K., Saito, D. and Takeda, K.  
TITLE Barley EST sequencing project in NIG and Okayama Univ  
JOURNAL Unpublished (2002)  
COMMENT Contact: Tadasu Shin-i  
Center for Genetic Resource Information  
National Institute of Genetics  
111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: tshin@genes.nig.ac.jp.

## FEATURES

source 1..556  
Location/Qualifiers  
/organism="Hordeum vulgare subsp. vulgare"  
/mol\_type="mRNA"  
/cultivar="Haruna Nijo"  
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/db\_xref="taxon:112509"  
/clone="bag823a09"  
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/clone\_lib="K. Sato unpublished cDNA library, cv. Haruna Nijo germination shoots"

## ORIGIN

Query Match 4.6%; Score 98.6; DB 9; Length 556;  
Best Local Similarity 96.2%; Pred. No. 2.4e-10;  
Matches 101; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1617 CACAGATACAGCGAATACAGAGAAATTCGTCGTATTTGACCAACATGAAGTGATT 1676  
21 CTACCGATACAGGAATACAGAGAAATTCGTCGTATTTGACCAACATGAAGTGATT 80  
QY 1677 GGAAGCATTTTCTCGTGTATGAAAAGCTTGATTTACCCGCAG 1721  
81 GGAAGCATTTTCTCGTGTATGAAAAGCTTGATTTACCCGCAG 125

RESULT 14 BQ240653 568 bp mRNA linear EST 03-MAY-2002  
LOCUS BQ240653 TaB05014F06R TaB05 Triticum aestivum cDNA clone TaB05014F06R, mRNA  
DEFINITION sequence.  
ACCESSION BQ240653  
VERSION BQ240653.1 GI:20436529  
KEYWORDS EST.  
SOURCE Triticum aestivum (bread wheat)

Mon Apr 12 10:24:23 2004

us-09-508-377-10\_copy\_1058\_3204.rst

Page 8

## ORGANISM

## REFERENCE

COMMENT

FEATURES  
source

ORIGIN

Query Match	4.6%	Score 98.6	DB 13	Length 568
Best Local Similarity	96.2%	Pred. No. 2.4e-10		
Matches 101	Conservative 0	Mismatches 4	Indels 0	Gaps 0

QY 1617 CAACGATACAGCGGAAATACAAAGAAATTCGTGCTGCTATGACCAACATGAAGTGCATT 16

Db 38 CTACCGATACAGGGAATTACAAGAGAAATTCGTGCTATGACCAACTTGAAGTGCATT 97

2y 1677 GGAAGCATTTTCTCGTGTATGAAAAAGCTTGGATTTTACCCGCAG 172  
 Db 98 GGAAGCATTTTCTCGTGTATGAAAAAGCTTGGATTTTACCCGCAG 142

RESULT 15  
BM368073

### DEFINITION

ACCESSION	BM368073
VERSION	BM368073.1
KEYWORDS	GI:181114635
SOURCE	EST.
ORGANISM	<i>Hordeum vulgare</i> subsp. <i>Hordeum vulgare</i> subsp.

REFERENCE	AUTHORS
1 (pages 1 to 139)	Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardie, L.,

JOURNAL Unpublished (2001)  
COMMENT Contact: Waugh R, Marshall DF

Tel: 00 44 1382 562731

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FEATURES
  source      location/Qualifiers
1. 1.139     mutation/20base substitution

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/lab_host="DH10B"
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/notes="Vector: pSPORT1; Site 1: Sal I; Site 2: Not I;
Non-normalised library, directionally cloned into pSPORT1.
Derived from endosperm tissue dissected from developing
grains (6 days post anthesis) in glasshouse grown barley
plants. Developed as part of the barley transcriptome
resources of BBSRC/BSERAD funded cereal IGF (Investigating
Gene Function) project."

```

## ORIGIN

Query Match	4.3%;	Score 92.6;	DB 12;	Length 139;
Best Local Similarity	90.2%;	Pred. No. 3.7e-09;		
Matches 11;	Conservative 0;	Mismatches 9;	Indels 3;	Gaps 1

Dy 161 GGGTCCGCGCAGCTCTGGGTGTGGCGCGGCCCGCGTCGAG---TGGCGCGGCGCG 217

Dd 1 GGGTCCGCGCAGCTCTGGGTGTGGCGCGGCCCGCGAGCGCTGCCTGGATCGG 60

Dy 218 CTGGAGCGGAGGGCGGGCGGAATTGCCGTCCGTCTCCTCAGAAAGAAGACCTCTC 277

Dz 61 CTCGAGCGGAGGGCGGGCTGCACTTGCCGTCCGTCTCCTCAGAAAGAAGACCTCTC 120

QY	278	TCG	280
Db	121	TCG	123

Search completed: April 10, 2004, 14:06:15  
Job time : 5678.27 secs

Tel: 00 44 1382 562731

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

## 3M nucleic - nucleic search, using sw model

Run on: April 10, 2004, 01:54:35 / Search time 8035.73 Seconds  
(without alignments)  
11057.263 Million cell updates/sec

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Perfect score: 2050  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues  
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
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2: gb\_hlg:\*  
3: gb\_in:\*  
4: gb\_cm:\*  
5: gb\_ov:\*  
6: gb\_ph:\*  
7: gb\_pl:\*  
8: gb\_pr:\*  
9: gb\_ro:\*  
10: gb\_sc:\*  
11: gb\_sy:\*  
12: gb\_un:\*  
13: gb\_vl:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
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25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sc:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_hlg\_hum:\*  
31: em\_hlg\_inv:\*  
32: em\_hlg\_other:\*  
33: em\_hlg\_mus:\*  
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36: em\_hlg\_mam:\*  
37: em\_hlg\_vrt:\*  
38: em\_sy:\*  
39: em\_higo\_hum:\*  
40: em\_higo\_mus:\*  
41: em\_higo\_other:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2050	100.0	11463	AX031271	AX031271 Sequence
2	2025	98.8	11475	AF338431	AF338431 Aegilops
3	250.8	12.2	691	AY235709	AY235709 Zea mays
4	250.8	12.2	693	AY235691	AY235691 Zea mays
5	250.8	12.2	693	AY235701	AY235701 Zea mays
6	250.8	12.2	712	AY235702	AY235702 Zea mays
7	250.8	12.2	713	AY235690	AY235690 Zea mays
8	250.8	12.2	713	AY235692	AY235692 Zea mays
9	250.8	12.2	713	AY235693	AY235693 Zea mays
10	250.8	12.2	713	AY235694	AY235694 Zea mays
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12	250.8	12.2	713	AY235696	AY235696 Zea mays
13	250.8	12.2	713	AY235697	AY235697 Zea mays
14	250.8	12.2	713	AY235698	AY235698 Zea mays
15	250.8	12.2	713	AY235703	AY235703 Zea mays
16	250.8	12.2	713	AY235704	AY235704 Zea mays
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18	250.8	12.2	713	AY235706	AY235706 Zea mays
19	250.8	12.2	713	AY235707	AY235707 Zea mays
20	250.8	12.2	713	AY235708	AY235708 Zea mays
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22	250.8	12.2	713	AY235712	AY235712 Zea mays
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29	240.4	11.7	651	AY2900243	AY2900243 Zea mays
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31	226.2	11.0	626	AY2900293	AY2900293 Zea mays
32	226.2	11.0	627	AY2900222	AY2900222 Zea mays
33	225.6	11.0	626	AY2900268	AY2900268 Zea mays
34	225.6	11.0	627	AY2900242	AY2900242 Zea mays
35	225.6	11.0	627	AY2900244	AY2900244 Zea mays
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37	225.6	11.0	626	AY2900215	AY2900215 Zea mays
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43	225	11.0	626	AY2900261	AY2900261 Zea mays
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## ALIGNMENTS

RESULT 1  
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DEFINITION Sequence 10 from Parent W09914314.  
ACCESSION AX031271  
VERSION AX031271.1 GI:10278603  
KEYWORDS  
SOURCE  
ORGANISM  
Aegilops tauschii  
Aegilops tauschii  
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,  
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,  
Poideae, Triticeae, Aegilops.  
REFERENCE  
Li, Z., Morell, M. and Rahman, S.  
1  
Regulation of gene expression in plants  
TITLE



## JOURNAL

Patent: WO 9914314-A 10 25-MAR-1999;  
GOODMAN FIELDER LTD (AU) ; LI ZHONGYI (AU) ;  
RAHMAN SABEQR (AU) ; UNIV AUSTRALIAN (AU) ; COMMW SCIENT IND RES  
ORG (AU) ; GROUPE LIVAGRAIN PACIFIC PTY L (AU)

## FEATURES

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QY 61 GGATACAAATGCAATGAGATATGCAATCCAGAGCAATTCATATGCAAGCTTTGGG 120  
DB 4878 GGATACAAATGCAATGAGATATGCAATCCAGAGCAATTCATATGCAAGCTTTGGG 4937  
QY 121 TATTCACAATCCATTTTCTGTATACACTTACCCATTGGAGCATTAACATCC 180  
DB 4938 TATTCACAATCCATTTTCTGTATACACTTACCCATTGGAGCATTAACATCC 4997  
QY 181 TATGCTCATGACATTAATAATTTGGATATATCTTATTAGATATATAGACAAT 240  
DB 4998 TATGCTCATGACATTAATAATTTGGATATATCTTATTAGATATATAGACAAT 5057  
QY 241 ACACTTAGATTTCTGAAAAAGATCATTTTATGTGTGGCTTTGCCAGGTACATGTT 300  
DB 5058 ACACTTAGATTTCTGAAAAAGATCATTTTATGTGTGGCTTTGCCAGGTACATGTT 5117  
QY 301 ACTAATTTTTTTGCAACAATAGCCGCTTTGGAACTCCAGAGCACTTAAATCCTTATC 360  
DB 5118 ACTAATTTTTTTGCAACAATAGCCGCTTTGGAACTCCAGAGCACTTAAATCCTTATC 5177  
QY 361 GATAGACACATGAGCTGTGGTTGCTGTCTTATGATATTTGTCATAGGTAATTAAGTC 420  
DB 5178 GATAGACACATGAGCTGTGGTTGCTGTCTTATGATATTTGTCATAGGTAATTAAGTC 5237  
QY 421 CAATTTAATTTAGCTGTTTAACTGTTTATCTGGTATTTCTAAAGGAAATTCAGGCAAT 480  
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QY 481 ATATATACATTTGCTAAAGCTTAAGGTGGCCAAATGCTCAAAATCTGAAGTGGAT 540  
DB 5298 ATATATACATTTGCTAAAGCTTAAGGTGGCCAAATGCTCAAAATCTGAAGTGGAT 5357  
QY 541 AAGGAAATTTGGCAAAACTAGAGTGGCAAAATTAATTTTCCATCCTTAATGGCAGG 600  
DB 5358 AAGGAAATTTGGCAAAACTAGAGTGGCAAAATTAATTTTCCATCCTTAATGGCAGG 5417  
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DB 5418 GCCCTATGCGCGAATATTTTTCATTTCTATATAAATTTGTGCTAGCTGACTTTTTCCTC 5477  
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QY 1321 TACTTGGTTGGTTGATTTCTATTTGATGTCAGTTGGTTCATCAATATTTGTGTACCT 1380  
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QY 1501 ATGGAGTTGGAAATGATGATGCTGACTTCGTGACCAATTTTGGCTAACTGTTCTC 1560  
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QY 1681 ACCCTCAGATGATATACACATGATTAACAAGTATGATCAAGGTTTCAGTAAT 1740  
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QY 1741 TTTTATGAGGCACTGAAACAAATGCTATGATCACTAAACATGATCATGATCAGGACTTGTG 1800  
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QY 1801 CTAAGAGTCTTATAGATGTTTCCCTAGATATGTTGTATCAATTTTAACCTGATGAGATCATGG 1860  
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QY 1861 AAGATTGGAAGTATATATTTATTTCTTTCTAGATTTGTTCTTCTTCTAGATGACA 1920  
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 Db 6738 TTACTGGGAACATATGCGCAATATTTGGATTTGCTACTGATGTTGATGCGGTAGTTAC 6797  
 2Y 1981 TTGATGCTGCTCAACGATCTAATTCATGAGCTTTATCTGATGCTATTCATTCGTGGA 2040  
 Db 6798 TTGATGCTGCTCAACGATCTAATTCATGAGCTTTATCTGATGCTATTCATTCGTGGA 6857  
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 Db 6858 GATGTAAGTG 6867

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 DEFINITION AF338431  
 ACCESSION AF338431 GI:13447949  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Aegilops tauschii  
 Aegilops tauschii  
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Poideae; Triticeae; Aegilops.  
 1 (bases 1 to 11475)  
 Rahman, S., Regina, A., Li, Z., Mukai, Y., Yamamoto, M.,  
 Kosar-Hademi, B., Abraham, S. and Morell, M.K.  
 Comparison of starch-branching enzyme genes reveals evolutionary  
 relationships among isoforms. Characterization of a gene for  
 starch-branching enzyme I1a from the wheat genome donor Aegilops  
 tauschii  
 Plant Physiol. 125 (3), 1314-1324 (2001)

JOURNAL MEDLINE 21140316  
 PUBMED 11244112  
 2 (bases 1 to 11475)  
 Rahman, S., Regina, A., Li, Z., Sharon, A. and Morell, M.K.  
 Direct Submission  
 Submitted (18-JAN-2001) Plant Industry, CSIRO, Clunies Rose,  
 Canberra, ACT 2601, Australia  
 Location/Qualifiers  
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 Best Local Similarity 99.8%; Pred. No. 0;  
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 Db 4881 GGATCAATGAGTGCAGATTAATGGCAATCCAGAGCATTCATATGCAAGCTTTGGG 4940  
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 180 CTATAGCTTCAGCAGATTAATTAATTTGATATATCCCTTATATATATATGTCACAC 229  
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 240 TACACTTAGATATCTG---AAAGAATCAATTTATTTGTTGGCTGTGCCAGTACCA 296  
 Db 5061 TACACTTAGATATCTGANNANNAAGATCAATTTATTTGTTGGCTGTGCCAGTACCA 5120  
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 417 AGTCATATTAATTTTAACTGTTTAACTGTTTAACTGTTTAACTGTTTAACTGAGC 476  
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 717 GTTCCATGAATATCGTTTGTAAATGCGCAACAAATTTGATGCGATAGATGAGATGAG 776  
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Db	624	TTGATGACCTTATCTGATGCTGATCCATTTGATGAGATGATAGT 671	
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ACCESSION	AY235701		
VERSION	AY235701.1	GI:30014025	
KEYWORDS			
SOURCE			
ORGANISM	Zea mays subsp. mays (maize)		
	Zea mays subsp. mays		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.		
REFERENCE	1 (bases 1 to 693)		
AUTHORS	Whitt,S.R., Wilson,L.M., Tenailon,M.I., Gaut,B.S. and Buckler,E.S.		
TITLE	Genetic diversity and selection in the maize starch pathway		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)		
MEDLINE	22247734		
PubMed	12244216		
REFERENCE	2 (bases 1 to 693)		
AUTHORS	Whitt,S.R., Wilson,L.M., Tenailon,M.I., Gaut,B.S. and Buckler,E.S.		
TITLE	Direct Submission		
JOURNAL	Submitted (11-FEB-2003) Genetics, USDA-ARS, North Carolina State University, 3513 Gardner Hall, Box 7614, Raleigh, NC 27655, USA		
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	Matches 461; Conservative 0; Mismatches 192; Indels 55; Gaps 4;		
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[illegible]

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RESULT 7
AY235690
LOCUS
DEFINITION
AY235690 713 bp DNA linear PLN 16-Apr-2003
Zea mays subsp. mays cultivar A272 amylose extender
starch-branching enzyme (ael1) gene, exons 12, 13, and 14 and
partial cds.
ACCESSION
AY235690
VERSION
AY235690.1 GI:30014003
KEYWORDS
SOURCE
ORGANISM
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Zea mays subsp. mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 713)
AUTHORS
Whitt,S.R., Wilson,L.M., Tenailon,M.I., Gaut,B.S. and Buckler,E.S.
GENETIC DIVERSITY AND SELECTION IN THE MAIZE STARCH PATHWAY
JOURNAL
PROC. NATL. ACAD. SCI. U.S.A. 99 (20), 12959-12962 (2002)
MEDLINE
22247734
PUBMED
12244216
REFERENCE
2 (bases 1 to 713)
Whitt,S.R., Wilson,L.M., Tenailon,M.I., Gaut,B.S. and Buckler,E.S.
IV.
Direct Submission
Submitted (13-FEB-2003) Genetics, USDA-ARS, North Carolina State
University, 3513 Gardner Hall, Box 7614, Raleigh, NC 27695, USA
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Best Local Similarity 65.1%; Pred. No. 1.7e-40;
Matches 461; Conservative 0; Mismatches 192; Indels 55; Gaps 4;

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79	TCTGATAGGGTTGATGGTTTGTATGGTACAGATACATTAATCTTCCACAGTGTCCAG	138
1463	CGGCCATCATTTGATGTGGGATTCCTGCTCAATTCATGATGGAGTTGGGAATGTGTAG	1522
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1583	GATATTCATTCCTATGACAGTATTTGAGATTCCTACTGTCAACGACGATGTGGCTTG	1642
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Db	564	ATTTCGCTTTGCCACCGATGATGATGAGTGTACTTACTGATGCTGGAATGATCTAA	623
QY	2003	TTTATGACTTTATCTGATGCTGATCCATTGCGAAGATCTAGTG	2050
Db	624	TTTATGACTTTATCTGATGCTGATGATGAGTGTAAAGATGTAAGTG	671
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DEFINITION		Zea mays subsp. mays cultivar B14a amylose extender	
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		partial cds.	
ACCESSION	AY235693		
VERSION	AY235693.1	GI:30014009	
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		Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD	
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REFERENCE		1 (bases 1 to 713)	
AUTHORS		Whitt,S.R., Wilson,L.M., Tenailon,M.I., Gaut,B.S. and Buckler,E.S.	
TITLE		Genetic diversity and selection in the maize starch pathway	
JOURNAL		Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)	
MEDLINE		22247734	
PUBMED		12244216	
REFERENCE		2 (bases 1 to 713)	
AUTHORS		Whitt,S.R., Wilson,L.M., Tenailon,M.I., Gaut,B.S. and Buckler,E.S.	
		IV.	
TITLE		Direct Submission	
JOURNAL		Submitted (13-FEB-2003) Genetics, USDA-ARS, North Carolina State	
		University, 5513 Gardner Hall, Box 7614, Raleigh, NC 27695, USA	
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Best local similarity		65.1%	Pred.No. 1.7e-40;



Best Local Similarity 65.1%; Pred. No. 1.7e-40;  
Matches 461; Conservative 0; Mismatches 192; Indels 55; Gaps 4;

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DEFINITION Zea mays subsp. mays cultivar B97 amylose extender starch-branching  
enzyme (ae1) gene, exons 12, 13, and 14 and partial cds.  
ACCESSION AY235696  
VERSION AY235696.1 GI:30014015  
KEYWORDS  
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ORGANISM  
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Zea mays subsp. mays  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 713)  
AUTHORS White,S.R., Wilson,L.M., Tenailion,M.I., Gaut,B.S. and Buckler,E.S.  
JOURNAL Genetic diversity and selection in the maize starch pathway  
Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)  
MEDLINE 22247734  
PUBMED 12244216  
REFERENCE 2 (bases 1 to 713)  
AUTHORS White,S.R., Wilson,L.M., Tenailion,M.I., Gaut,B.S. and Buckler,E.S.

IV.  
TITLE Direct Submission  
JOURNAL Submitted (13-FEB-2003) Genetics, USDA-ARS, North Carolina State  
University, 3513 Gardner Hall, Box 7614, Raleigh, NC 27695, USA  
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Best Local Similarity 65.1%; Pred. No. 1.7e-40;  
Matches 461; Conservative 0; Mismatches 192; Indels 55; Gaps 4;  
QY 1343 TTGAGTTCATGCTGCTCAATGATTTTGTGTCACCCGACATGATTCGTCGAATATAC 1402  
Db 19 TTGGTTTCAATACCTTTAATCTTTGTTGTATCTTGACAGTACGCTCAAGTAAATAC 78  
QY 1403 CCTGACCGGTTTGAATGTTTGCATGACGACTATACATTAATCTTCCAGGTGCTCAG 1462  
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Db	481	ATATTGTTATATATCATTCCTCTTTCTAACTAAAGCA-----	520
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Qy	1943	ATTTTGGATTGCTACTGATGTTGATGGGAGTATTACTTGATGCTGCTCAACGATCTAA	2002
Db	564	ATTTTGGCTTTGCCACCGATGATAGTAGAGTGTTACTTATGCTGTAAATGATCTAA	623
Qy	2003	TTCATGACATTATCTGATGATGCTGATTCATGTGTGAAAGTGAAGT	2050
Db	624	TTTCATGACATTATCTGATGAGGCTGTAACCATGTGTGAAGAGTGAAGT	671

RESULT 13	LOCUS	DEFINITION	GI:30014017
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AY235697	AY235697		
AY235697.1	AY235697.1		GI:30014017

SOURCE ORGANISM	Substrate	Enzyme
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<i>Zea mays</i> subsp. <i>mays</i>	Starch	α-amylase

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

**AUTHORS** White, S.R., Wilson, L.M., Tenallion, M.I., Gaut, B.S. and Buckler, E.S.  
**TIME** Genetic diversity and selection in the maize starch pathway  
**JOURNAL** Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12859-12962 (2002)

PUBMED  
12244216  
REFERENCE  
2 (Pages 1 to 713)  
AUTHORS  
Whitt, S.R., Wilson, L.M., Tenailon, M.I., Gaut, B.S. and Buckler, E.S

TITLE	Direct Submission
JOURNAL	Submitted (11-FEB-2003) Genetics, USDA-ARS, North Carolina State University, 3513 Gardner Hall, Box 7614, Raleigh, NC 27695, USA
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Best Local Similarity	65.1%	Pred. No.	1.7e-40				
Matches	461	Conservative	0	Mismatches	192	Indels	55
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RESULT 14  
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 LOCUS  
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 AY235698 713 bp DNA linear PLN 16-APR-2003  
 Zea mays subsp. mays cultivar CML254 amylose extender  
 starch-branching enzyme (aet) gene, exons 12, 13, and 14 and  
 partial cds.  
 AY235698  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
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 Zea mays subsp. mays  
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 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 713)  
 White,S.R., Wilson,L.M., Tenailon,M.I., Gaut,B.S. and Buckler,E.S.  
 Genetic diversity and selection in the maize starch pathway  
 Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)  
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PUBMED 12244216  
2 (bases 1 to 713)  
REFERENCE White,S.R., Wilson,L.M., Tenailon,M.I., Gaut,B.S. and Buckler,E.S.  
AUTHORS IV.  
TITLE Direct Submission  
JOURNAL Submitted (13-FEB-2003) Genetics, USDA-ARS, North Carolina State  
University, 3513 Gardner Hall, Box 7614, Raleigh, NC 27695, USA  
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ORIGIN

Query Match 12.2%; Score 250.8; DB 8; Length 713;  
Best Local Similarity 65.1%; Pred. No. 1.7e-40;  
Matches 461; Conservative 0; Mismatches 192; Indels 55; Gaps 4;

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Db 19 TTGGTTTCAACCTTAACCTTGTCTTTGTCTTACTTCAGTCATTCGTCAAAATATAC 78  
QY 1403 CTTGACGGTTTGAATGGTTTGATGGACCTGATACACATTACTTCACGGTGTCCAGC 1462  
Db 79 TCTGGATGGTTGAATGGTTTGATGGATGATACACATTACTTCACAGTGTCCAGC 138  
QY 1463 CGGCATATATGATGTGGGATTTCTCGTATATCAACTATGGAGTTGGAAATATAGTAG 1522  
Db 139 TGGCCATACCTGAGATGGGATTTCTCGCTATTATTAATGGAACCTGGAAATAG--G 196  
QY 1523 CTCGACTTCCTGTCACCAATATTTGGCTAATCTGCTCTTAATCTGCTTACACATGT 1582  
Db 197 AACCAAAATGCTCTATCTCCATTAATTTATCTCTTATTTTTCCTGATCATTCACA 256  
QY 1583 GATAATTCATTTCTTATGACAGATATGAGATCTTACTGTCAACCGGAGATGGTGGCTTG 1642  
Db 257 ACAATTTATCGGATGACAGGTTTAAAGATTTCTTCTCCAAATGCTAAGTGGTGGCTG 316  
QY 1643 AAGATATATAGTTTATGATTTTCATTTGATGGGGTGAACCTCCAGATGATATACAC 1702  
Db 317 AGGATATATAGTTTATGATTTTCGTTTGAATGGTGTGACCTCCAGATGATATACAC 376  
QY 1703 ATGATTAACAAGTAAGTCATCAAGTGGTTTCAGTAACTTTTAAAGGGCACTGAAACAT 1762  
Db 377 ACGGATTAACAAGTAATTTAAGCTTTATGCTCTGTATTTATCT-----TCACTGCTA 429  
QY 1763 GCTATGATCATATACATGATATGATCAAGACTTGTGCTACGAGCTTTAGATAGTTCC 1822

Db 430 AGTCTGACTGGAATACTGATTTATGCTGGAACT-----AGTTTGTATGATAC 480  
QY 1823 CTAGTATGCTGTGACAAATTTTAACTGATGATGATGATGGAAGTATATAT 1882  
Db 481 ATATTTGTATATATATCTCTCTTTCTTATCTTAAGCA----- 520  
QY 1883 TATTTCTTTCTTAAGTTTGTCTTGTCTTATGATGACATTTTACGGAATGCGAAT 1942  
Db 521 -----TCAATTTACTTTTGTATACATTTACGGGAATCTCAATGAGT 563  
QY 1943 ATTTTGAATTTGCTACTGATGATTTATGCGGATGATTTACTTATGCTGTCACGATCTA 2002  
Db 564 ATTTTGGCTTTGACACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 623  
QY 2003 TTCAATGACTTTATCTCGATGCTGATTCATTCATTTGATGATGATGATGATGATG 2050  
Db 624 TTCAATGACTTTATCTCTGAGGCTTAAACATTTGATGATGATGATGATGATG 671

RESULT 15  
AY235703  
LOCUS  
DEFINITION  
Zea mays subsp. mays cultivar IDS28 amylose extender starch-branching enzyme (ae1) gene, exons 12, 13, and 14 and partial cds.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Zea mays subsp. mays (maize)  
Zea mays subsp. mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
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REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
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LMLVNDLHGLYPRAVTIGEDV"  
61..190  
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ORIGIN  
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Query Match      12.28; Score 250.8; DB 8; Length 713;
Best Local Similarity 65.18; Pred. No. 1.7e-40;
Matches 461; Conservative 0; Mismatches 192; Indels 55; Gaps 4;

QY 1343 TTGAGTTCATGCTTCATCAATGATTTTGTGACCCGACGATTCGTCAATAATATAC 1402
DB 19 TTTGGTTTCATCTTTAACTTTGCTTTTGTGTTACTTGCATGCTAGGTCAAGTAATAC 78
QY 1403 CCTTGAAGGTTGAATGTTTGAATGGCACTGATACAACTTCCACGGTGTCCACG 1462
DB 79 TCTGATGGGTTGAATGTTTGTGATGTACAGATACAACTTCCACAGTGTCCACG 138
QY 1463 CGGCCATCATGATGATGGGATTTCTGCTATTTCACTATGGAGTGGGAAGTATGTAG 1522
DB 139 TGGCCATCACTGATGATGGGATTTCTGCTATTTCACTATGGAGTGGGAAGTACG--G 196
QY 1523 CTCTGACTTCTGTACCATATTTGGCTAAGTTCCTGTTAATCTGTTCCTTACACATGTT 1582
DB 197 AACAAAATCTCTATCTCATTTATTTATCTCTATTTTCTGCTGTATGCTTCCA 256
QY 1583 GATATTTCTATTTCTTATGAGGATTTGAGATTTCTACTGTCAACGCGAGATGTGCTTG 1642
DB 257 ACAATTTTATCCGATGCAAGTTTGAATTTCTTCTCCAAATGCTAGATGTGCTCG 316
QY 1643 AAGAAATATAGTTGATGAGATTTTGATTTGATGGGTGACCTCCATGATGTAATCAAC 1702
DB 317 AGGAATATATAGTTGATGAGGTTTCCGTTTGAATGATGACCTCCATGATGTAATCAAC 376
QY 1703 ATGATTTTACAAGTAAAGCATCAAGTGTTCAGTAACTTTTATAGGCACTGAAACAAT 1762
DB 377 ACGGATTTACAAGTAAATTAAGCTTTATGCTGTTAGTTATCT-----TCACTGTGCTA 429
QY 1763 GCTATGCAATCAACAATGATGATGATGATGAGACTTGTGCTACGAGTCTTAGATAGTTCC 1822
DB 430 AGTCTACTGGAATGATGATGATGATGCTGGAAGT-----AGTTTGTTAGTATC 480
QY 1823 CTAGTATGCTTGAACAATTTTAACTGATGATGATGATGGAAGATGGAAGTATTTATT 1882
DB 481 ATATTTGTATATATATCATCTCTTCTTCTTAACTAAAGTCA----- 520
QY 1883 TATTTCTTCTAAAGTTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1942
DB 521 -----TGCATTTTACTTTTGTAGTAACTTTTACGGGGAAGTCAATGAGT 563
QY 1943 ATTTGGAATTTGCTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2002
DB 564 ATTTGGAATTTGCTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 623
QY 2003 TTGATGACTTTTATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2050
DB 624 TTGATGACTTTTATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 671
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Search completed: April 10, 2004, 10:02:27  
Job time : 8044.07 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 10, 2004, 01:51:55 ; Search time 802.094 Seconds  
(without alignments)  
10857.595 Million cell updates/sec

Title: US-09-508-377-10\_COPY\_4818\_6867

Sequence: 1 ccgaagataaattcattatgc.....cattgtgaagatgtaagt 2050

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: N\_Geneseq\_230a04:\*

1: Geneseq1980s:\*\n2: Geneseq1990s:\*\n3: Geneseq2000s:\*\n4: Geneseq2001as:\*\n5: Geneseq2001bs:\*\n6: Geneseq2002s:\*\n7: Geneseq2003as:\*\n8: Geneseq2003bs:\*\n9: Geneseq2003cs:\*\n10: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2050	100.0	11473	2	AAx34650 Search br
2	2025	98.8	11475	5	AAH78338 Nucleotid
3	250.8	12.2	23449	3	AAZ25393 Maize amy
4	241.2	11.8	8381	5	AAH78343 Partial g
5	141	6.9	2726	5	AAH78337 Nucleotid
6	126.2	6.2	11473	2	AAx34650 Search br
7	126.2	6.2	11473	5	AAH78338 Nucleotid
8	122.8	6.0	2304	9	ADCO8218 Rice DNA
9	122.8	6.0	2655	7	ADA71289 Rice gene
10	122.8	6.0	3015	2	AAV05639 Rice type
11	119.2	5.8	2307	9	ADCO7807 Rice DNA
12	110.6	5.4	2087	2	AAI69737 Corn star
13	110.6	5.4	2165	2	AAI69736 Corn star
14	110.6	5.4	2640	2	AAV70961 DNA encod
15	110.6	5.4	2665	2	AAI69729 plasmid p
16	110.6	5.4	2725	2	AAV29757 Zea may
17	108.4	5.3	2000	7	ADA72630 Rice gene
18	108.2	5.3	2919	3	AAQ73750 Rice star
19	105	5.1	2307	2	AAZ29938 DNA encod
20	105	5.1	2968	5	AAH78342 Nucleotid
21	105	5.1	3039	6	ABK15494 Wheat sct
22	102.2	5.0	7800	9	ADB84160 Gene expr

24	95.4	4.7	1919	2	AAV38722 cDNA enco
25	94.8	4.6	3033	2	AAT42630 Class A s
26	94	4.6	2563	5	ABK50301 Potato cd
27	94	4.6	2576	2	AAT42636 Class A s
28	94	4.6	2578	2	AAT42631 Class A s
29	94	4.6	3003	2	AAT42634 Class A s
30	94	4.6	3074	2	AAT42637 Class A s
31	93.6	4.6	303	7	ABX87740 Corn ear-
32	93.6	4.6	7800	9	ADB84160 Gene expr
33	93	4.5	2000	7	ADA72281 Rice gene
34	92.4	4.5	2529	2	AAT42637 Class A s
35	92.4	4.5	2531	2	AAT17267 Class A s
36	92.4	4.5	2975	2	AAT42635 Class A s
37	92	4.5	2000	7	ADA72423 Rice gene
38	91.8	4.5	2000	7	ADA72699 Rice gene
39	91.4	4.5	2000	7	ADA72630 Rice gene
40	91.2	4.4	2000	7	ADA72699 Rice gene
41	90.8	4.4	3090	2	AAV38720 Full leng
42	90.8	4.4	258	3	AAI67269 Pinus rad
43	90.8	4.4	3231	2	AAT42632 Class A s
44	90.6	4.4	2000	7	ADA72110 Rice gene
45	90	4.4	2000	7	ADA72991 Rice gene

## ALIGNMENTS

RESULT 1  
ID AAX34650 standard; DNA; 11473 BP.  
AC AAX34650;  
XX  
DT 17-OCT-2003 (revised)  
DT 05-JUL-1999 (first entry)  
XX  
DE Search branching enzyme II (SBE II) gene sequence.  
XX  
XX Search biosynthetic pathway; cereal plant; enzyme; SBE; SSS; DBR; GBS;  
XX search branching enzyme; starch soluble synthase; debanching enzyme;  
XX endosperm; wheat; barley; granule-bound synthase; glutenn; starch;  
XX grain scutness protein I; bacterial isomylase; glycogen synthase;  
XX WBE I-D4 gene; ss.  
XX  
XX Aegilops tauschii.  
XX  
XX PN WO9914314-A1.  
XX  
XX PD 25-MAR-1999.  
XX  
XX PF 11-SEP-1998; 98MO-AU000743.  
XX  
XX PR 12-SEP-1997; 97AU-00009108.  
XX  
XX PR 20-MAR-1998; 98AU-00002509.  
XX  
XX PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
XX (AUSU ) UNIV AUSTRALIAN NAT.  
XX (GOOD-) GOODMAN FIELDER LTD.  
XX (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.  
XX  
XX PA Li Z, Moresl M, Rahman S;  
XX  
XX PI WPI; 1999-229525/19.  
XX  
XX DR New isolated cereal plant enzyme genes used for, e.g. expression of  
XX antienase sequences of granule bound synthase.  
XX  
XX PT Claim 8; Page 75-81; 17pp; English.  
XX  
XX PS The invention relates to a novel enzyme of starch biosynthetic pathway in  
XX a cereal plant, where the enzyme is selected from starch branching enzyme  
XX (SBE) I, SBE II, starch soluble synthase (SSS) I, and debanching enzyme



rice or maize. The methods and products can be used for targeting expression specifically to the endosperm of the seeds of cereal plants such as wheat or barley. They can be used for the expression of e.g. antisense sequences of granule-bound synthase (GBS), SBE II, low mol. wt. glutenin, grain softness protein 1, bacterial isomylase, bacterial glycogen synthase, and wheat high mol. wt. glutenin Bx17. They can be used for modifying the characteristics of starch produced by a plant. The present sequence represents the SBE II gene sequence. (updated on 17-Oct-2003 to standardise OS field)

Sequence 11473 BP; 3096 A; 2263 C; 2423 G; 3691 T; 0 U; 0 Other;

Query Match 100.0%; Score 2050; DB 2; Length 11473;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2050; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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4828 CCGAAGATTAATTCATATGCTAATTTTGGAGTAGAGGTGGCCAGAAATTAAGGCTT 4887  
61 GGATACATGCAAGTGCAGATTAATGCAATCAGAGGATTCATATGCAAGCTTTGGG 120  
4888 GGATACATGCAAGTGCAGATTAATGCAATCAGAGGATTCATATGCAAGCTTTGGG 4947  
121 TATTCACACATTCATTTTCTGTATACACTCTTACCCATTTGGAGCTATTAATCC 180  
4948 TATTCACACATTCATTTTCTGTATACACTCTTACCCATTTGGAGCTATTAATCC 5007  
181 TATATGTTATGACATTAATAATTGGATATATCTTATAGATATATAGACACT 240  
5008 TATATGTTATGACATTAATAATTGGATATATCTTATAGATATATAGACACT 5067  
241 AACACTTATTTCTGAAAAAGATCATTTTATGTTGTGCTGTTCCAGGTACCATGTT 300  
5068 AACACTTATTTCTGAAAAAGATCATTTTATGTTGTGCTGTTCCAGGTACCATGTT 5127  
301 ACTAATTTTTCGACCAAGTACCCGTTTGGAACTCCAGAGACTTAATAATCCTTGATC 360  
5128 ACTAATTTTTCGACCAAGTACCCGTTTGGAACTCCAGAGACTTAATAATCCTTGATC 5187  
361 GATAGACACATAGGCTGTTGCTGTTCTTATGATATGTTCTCATAGGTAATTAATC 420  
5188 GATAGACACATAGGCTGTTGCTGTTCTTATGATATGTTCTCATAGGTAATTAATC 5247  
421 CAATTTAATTTAGCTGTTTAACTGTTTATCTGTTATCTGATTTCTAAGGAAATTCAGGCAATT 480  
5248 CAATTTAATTTAGCTGTTTAACTGTTTATCTGTTATCTGATTTCTAAGGAAATTCAGGCAATT 5307  
481 ATATATCATTTGTCAAAAAGCTTAAGAGTGGCGAAAGTGAATGTCAAATCTTGAATGGCAT 540  
5308 ATATATCATTTGTCAAAAAGCTTAAGAGTGGCGAAAGTGAATGTCAAATCTTGAATGGCAT 5367  
541 AAGGAAATTTGGCAAAAACCTAGAGTGGCAAAAATTAATAATTTCCCATCTTAATGGCAGG 600  
5368 AAGGAAATTTGGCAAAAACCTAGAGTGGCGAAATTAATAATTTCCCATCTTAATGGCAGG 5427  
601 GCCCTATGCGGCAATATTTTTCATTTCTATATAAATGTTGCTAGCTGATCTTTTCTG 660  
5428 GCCCTATGCGGCAATATTTTTCATTTCTATATAAATGTTGCTAGCTGATCTTTTCTG 5487  
661 AGATGATTTAAACCAAGTGGACATGAATATGTTTGGACATGTATGAATTAATGACAGTTC 720  
5488 AGATGATTTAAACCAAGTGGACATGAATATGTTTGGACATGTATGAATTAATGACAGTTC 5547  
721 CATAGAAATATGTTTGTATAGCAACAATTTGATGCTATAGATGATGATGATGATGAT 780  
5548 CATAGAAATATGTTTGTATAGCAACAATTTGATGCTATAGATGATGATGATGATGAT 5607  
781 TCAGATGCTATCAATAGAAATTAATCAATGCGCATGATCTGCGGCACTACATATAGTTT 840  
5608 TCAGATGCTATCAATAGAAATTAATCAATGCGCATGATCTGCGGCACTACATATAGTTT 5667

5668 GCAAGTTGAAAACTGACAGCAATTCCTCATCGTAATAGGCGCAGGCCCATCTGCGCAG 5727  
901 TTCAATAGATGTTACTTCCCTGTTGAATTCATTTGAACATATTAATCTTAAAGTTCTTCA 960  
5728 TTCAATAGATGTTACTTCCCTGTTGAATTCATTTGAACATATTAATCTTAAAGTTCTTCA 5787  
961 TTGTGCTTAAGTCAACTCTTTTAAGTTTGAACCAAGTCAATTTGAAATATATCAATC 1020  
5788 TTGTGCTTAAGTCAACTCTTTTAAGTTTGAACCAAGTCAATTTGAAATATATCAATC 5847  
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5848 TACAACACCAATTAATCTTATGATAGATTAACAATTTTATTTATTTATTTAGACATCT 5907  
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5908 TTGATGTTGATATGACACATTTTCTATAGACTTGTCAATATAGAGAACTTTGA 5967  
1141 CTTAGACAAATCTAGAACTTCAATCAATTTGGATCAGAGGAAACATCAATATATAGA 1200  
5968 CTTAGACAAATCTAGAACTTCAATCAATTTGGATCAGAGGAAACATCAATATATAGA 6027  
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6028 TAGATGTCACACCTTCAACAAAAATCAGACCTTGTCCACATATATGATCAGACCATC 6087  
1261 TGTGTTGCTTACGACCTTGTCTTCAATTTATGTTGTGATCTTAATCTTCTTCTTC 1320  
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1321 TACTTGTGTTGTTGATTCATATTTAGTTGCAATGCTTCCATCAATAGATTTTGGTACCT 1380  
6148 TACTTGTGTTGTTGATTCATATTTAGTTGCAATGCTTCCATCAATAGATTTTGGTACCT 6207  
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6208 GCAAGCATTTCTCAAAATATACCTTGCAGGTTTGAATGTTTGCATGCGACATGATAC 6267  
1441 ATTACTTCCAGGTTGTCAGGCGGCGCATTTGATGATGATGATGATGATGATGAT 1500  
6268 ATTACTTCCAGGTTGTCAGGCGGCGCATTTGATGATGATGATGATGATGATGAT 6327  
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6328 ATGGAGTTGGAAAGTATATGATGCTGCACTTGTGCAATATTTGGGTAATCTGCTG 6387  
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6388 TTAATCTGTTCTTACACATGTTGATATTTCTATCTTATGAGGATTTGATCTTAATC 6447  
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6448 TCAAAACGGAAGTGTGCTTGAAGAAATTAAGTTGATGATTTGATTTGATGATG 6507  
1681 AACTTCATGATATATACCAATGATGATGATGATGATGATGATGATGATGATGAT 1740  
6508 AACTTCATGATATATACCAATGATGATGATGATGATGATGATGATGATGATGAT 6567  
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1801 CTACGAGAGCTTATAGATTTCCCTATGATGATGATGATGATGATGATGATGATG 1860  
6628 CTACGAGAGCTTATAGATTTCCCTATGATGATGATGATGATGATGATGATGATG 6687  
1861 AAGATTGGAAGATTAATATTTATTTCTTCTTCAAGTTGTTGTTGTTGTTGTTGTT 1920  
6688 AAGATTGGAAGATTAATATTTATTTCTTCTTCAAGTTGTTGTTGTTGTTGTTGTT 6747  
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Db 6748 TTTACTGGGAAGCTATGGGGAATATTTTGGATTGCTACTGATGATTTGGAGGTAAGTTAC 6807  
QY 1981 TTGATGCTGTGCAACGATCTAATTCATGAGACTTTATCTGATGCTGATCATTTGGTGAA 2040  
Db 6808 TTGATGCTGTGCAACGATCTAATTCATGAGACTTTATCTGATGCTGATCATTTGGTGAA 6867  
QY 2041 GATGTAAGTG 2050  
Db 6868 GATGTAAGTG 6877

RESULT 2  
AAH78338

ID AAH78338 standard; CDNA; 11475 BP.

AAH78338;

26-NOV-2001 (first entry)

Nucleotide sequence of a starch branching enzyme designated F2.

wheat; starch branching enzyme; BE1b; SBE; transgenic plant;

starch biosynthetic pathway; amylopectin; F2; amylose; ss.

Aegilops tauschii.

MO200162934-A1.

30-AUG-2001.

21-FEB-2001; 2001MO-AUD00175.

21-FEB-2000; 2000AU-00005742.

(CSIR) COMMONWEALTH SCI & IND RES ORG.

(GOOD-) GOODMAN FIELDER LTD.

(LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.

Morell M, Rahman S;

WPI; 2001-570635/64.

Nucleic acid encoding wheat starch branching enzyme 1b, useful for

altering the amylose and amylopectin content of cereal plants, e.g. wheat

and barley.

Example 1; Fig 2; 103pp; English.

The present sequence encodes a wheat starch branching enzyme of Aegilops  
tauschii, designated F2. A. tauschii is likely to be the ancestral D  
genome donor of wheat. Probes isolated from the present sequence were  
used to identify type II starch branching enzymes (SBEs) in wheat,  
especially BE1b. The BE1b nucleic acids may be used to genetically  
transform cereal plants such as wheat or barley and for altering their  
nutritional content by modulating the starch biosynthetic pathway to vary  
levels of amylopectin and/or amylose produced in the plant

Sequence 11475 BP; 3093 A; 2259 C; 2423 G; 3689 T; 0 U; 11 Other;

Query Match 98.8%; Score 2025; DB 5; Length 11475;

Best Local Similarity 99.8%; Pred. No. 0; Mismatches 1; Indels 4; Gaps 2;

Matches 2049; Conservative 0; Mismatches 1; Indels 4; Gaps 2;  
QY 1 CCGAAGATAAATTCATATGCTAATTTTGGGATGAGGTGTCGCAAGATTAAAGGCTT 60  
Db 4821 CCGAAGATAAATTCATATGCTAATTTTGGGATGAGGTGTCGCAAGATTAAAGGCTT 4880  
QY 61 GGATACATGAGTGCAGATATATGGCAATCCAGAGCATTCATATGCAAGCTTTGGG 120  
Db 4881 GGATACATGAGTGCAGATATATGGCAATCCAGAGCATTCATATGCAAGCTTTGGG 4940  
QY 121 TATTCAACATCCATTTTTCCTGTTATAGAC-TCTTCAACCATTTGGAGCATATGATC 179

Db 4941 TATTCAACATCCATTTTTCCTGTTATAGACANTCTCACCCATTTGGAGCATATGATC 5000  
QY 180 CTATGCTTCATGACATATAAATTTTGGATATATATCTTTATATAGATATATGATACAC 239  
Db 5001 CTATGCTTCATGACATATAAATTTTGGATATATATCTTTATATAGATATATGATACAC 5060  
QY 240 TACACTTAGATCTG---AAAAAGATCATTTATTTGTTGGCTTGTCCAGGTACCA 296  
Db 5061 TACACTTAGATCTG---AAAAAGATCATTTATTTGTTGGCTTGTCCAGGTACCA 5120  
QY 297 TGTACTAATTTTGTGCAACCAAGTAGCCGTTTGGAACTCCAGAGCATTTAAATCCTT 356  
Db 5121 TGTACTAATTTTGTGCAACCAAGTAGCCGTTTGGAACTCCAGAGCATTTAAATCCTT 5180  
QY 357 GATGATAGAGCATAGAGCTTGGTTGCTTGTCTTATGGAATTTGTTCAATAGTAAT 416  
Db 5181 GATGATAGAGCATAGAGCTTGGTTGCTTGTCTTATGGAATTTGTTCAATAGTAAT 5240  
QY 417 AGTCCAAATTAATTTAGCTGTTTACTGTTTATCTGATCTGATCTTAAAGGAAATTCAGGC 476  
Db 5241 AGTCCAAATTAATTTAGCTGTTTACTGTTTATCTGATCTTAAAGGAAATTCAGGC 5300  
QY 477 AATTATGATCATTTGTCMAAAGCTAAGAGTGGCGMAAGTGAATGTCAAAATCTAGAGTG 536  
Db 5301 AATTATGATCATTTGTCMAAAGCTAAGAGTGGCGMAAGTGAATGTCAAAATCTAGAGTG 5360  
QY 537 GCATTAAGAAAATTGGCAAAAACCTAGAGTGGCAAAAATTAATTTTCCATCTTAATG 596  
Db 5361 GCATTAAGAAAATTGGCAAAAACCTAGAGTGGCAAAAATTAATTTTCCATCTTAATG 5420  
QY 597 CAGGGCCCTATGGCCGAATTTTTCATCTGATATATATGTTGCTAGCGTCTTCTT 656  
Db 5421 CAGGGCCCTATGGCCGAATTTTTCATCTGATATATATGTTGCTAGCGTCTTCTT 5480  
QY 657 TCTCAGATGATTAATAACAGATGAGCATGAAATGTATTTGGTACATGATGATACTGACA 716  
Db 5481 TCTCAGATGATTAATAACAGATGAGCATGAAATGTATTTGGTACATGATGATACTGACA 5540  
QY 717 GTTCCATAGAAATTCGTTTGTATAGGCAACAATTTGATGCCATGATGATGATG 776  
Db 5541 GTTCCATAGAAATTCGTTTGTATAGGCAACAACAATTTGATGCCATGATGATGATG 5600  
QY 777 AAGTTAGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 836  
Db 5601 AAGTTAGATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5660  
QY 837 GTTTCAGAGTTGGAAAACCTGACAGCAATACCTCATGATGATGATGATGATGATGATG 896  
Db 5661 GTTTCAGAGTTGGAAAACCTGACAGCAATACCTCATGATGATGATGATGATGATGATG 5720  
QY 897 CAGCTTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 956  
Db 5721 CAGCTTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5780  
QY 957 TTTATTTGCTTAAGTCAAACTCTTAAATTTGACCAAGTCTATTTGGAATAATATGAA 1016  
Db 5781 TTTATTTGCTTAAGTCAAACTCTTAAATTTGACCAAGTCTATTTGGAATAATATGAA 5840  
QY 1017 CATCTCAACACCAAAATTTATCTTATGATGATGATGATGATGATGATGATGATGATGATG 1076  
Db 5841 CATCTCAACACCAAAATTTATCTTATGATGATGATGATGATGATGATGATGATGATGATG 5900  
QY 1077 ATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1136  
Db 5901 ATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5960  
QY 1137 TTGACTTAGAGCAAACTGGAATCTTCAATCAATTTTGGATGAGAGGAAATCAATCAATATA 1196  
Db 5961 TTGACTTAGAGCAAACTGGAATCTTCAATCAATTTTGGATGAGAGGAAATCAATCAATATA 6020  
QY 1197 TAGATAGATGCAACCTTCACAAAATAATGACCTTGTGACCAATATGATGATGATGATG 1256

QY	1257	CATCTGTTTGGCTTTAGCCACTTCCTTCATATTATGTTGGTACCTAAATCTACTTTTC	1316	FT	Key	Location/Qualifiers
DB	6081	CATCTGTTTGGCTTTAGCCACTTCCTTCATATTATGTTGGTACCTAAATCTACTTTTC	6140	FT	misc_signal	597..602
QY	1317	CTTCTTACTGGTTTGGTTGATTTCTATTTCAGTTGCATTTGCTTCAATGATTTTGGTGA	1376	FT	repeat_unit	/tag= a /note= "I box, conserved in RBCs genes"
DB	6141	CTTCTTACTGGTTTGGTTGATTTCTATTTCAGTTGCATTTGCTTCAATGATTTTGGTGA	6200	FT	misc_signal	1475..1481
QY	1377	CCCTGAGTCATTCGTCAAATTAATACCCCTGACGGTTGATGGTTGCGATGGCAGTAT	1436	FT	misc_signal	/tag= b /note= "RY repeat, distal regulatory element"
DB	6201	CCCTGAGTCATTCGTCAAATTAATACCCCTGACGGTTGATGGTTGCGATGGCAGTAT	6260	FT	misc_signal	1967..1973
QY	1437	ACACATTACTTCCACGAGTGTGTCACGCGGCATTCATGATGGATTCGTCTATTC	1496	FT	GC_signal	/tag= c /note= "Hex, conserved element found in plant histone gene promoters"
DB	6261	ACACATTACTTCCACGAGTGTGTCACGCGGCATTCATGATGGATTCGTCTATTC	6320	FT	GC_signal	2593..2599
QY	1497	AACATAGGAGTTGGGAAGTATGATGCTGACTTCTGTCAACCATTTTGGCTAACTGTT	1556	FT	GC_signal	/tag= d /note= "MRE box, motif essential for metal ion-dependent induction of metallothionein genes"
DB	6321	AACATAGGAGTTGGGAAGTATGATGCTGACTTCTGTCAACCATTTTGGCTAACTGTT	6380	FT	GC_signal	2666..2671
QY	1557	CCGTAAATCTGTTCTTACACATGTTGATATTCATTCATTCGAGGATTTGAGATTTCTT	1616	FT	misc_signal	/tag= e 2738..2743
DB	6381	CCGTAAATCTGTTCTTACACATGTTGATATTCATTCATTCGAGGATTTGAGATTTCTT	6440	FT	GC_signal	/tag= f 2831..2836
QY	1617	ACTGTCAACGCGAGATGCTGCTGAGAATAATAGTTGATGATTTGCATTTGATG	1676	FT	GC_signal	/tag= g 2838..2844
DB	6441	ACTGTCAACGCGAGATGCTGCTGAGAATAATAGTTGATGATTTGCATTTGATG	6500	FT	TATA_signal	/tag= h /note= "MRE box, motif essential for metal ion-dependent induction of metallothionein genes"
QY	1677	GGTGACCTCCATGATGATTAATCAATGATTTCAAGTGAAGTGAAGTGAAGTGAAGT	1736	FT	exon	2933..2936
DB	6501	GGTGACCTCCATGATGATTAATCAATGATTTCAAGTGAAGTGAAGTGAAGTGAAGT	6560	FT	exon	/tag= i 2965..3176
QY	1737	AACATTTTAAAGGACATGGAACAATTCCTAATGATTCATACATGATCATGACGACT	1796	FT	CDS	/tag= j /number= 1 3065..19659
DB	6561	AACATTTTAAAGGACATGGAACAATTCCTAATGATTCATACATGATCATGACGACT	6620	FT	intron	/tag= k /note= "contains introns"
QY	1797	TGTGCTACGAGTCTTATGATGATTCCTAGTATCTGTACAAATTTTACCTGATGAGATC	1856	FT	exon	/tag= l /number= 1 3283..3428
DB	6621	TGTGCTACGAGTCTTATGATGATTCCTAGTATCTGTACAAATTTTACCTGATGAGATC	6680	FT	intron	/tag= m /number= 2 3429..3672
QY	1857	ATGGAAGATTGGAAGTATTAATTTATTTCTTCTAAGTTGTTCTTCTGTTAGAT	1916	FT	intron	/tag= n /number= 2 3673..3827
DB	6681	ATGGAAGATTGGAAGTATTAATTTATTTCTTCTAAGTTGTTCTTCTGTTAGAT	6740	FT	exon	/tag= o /number= 3 3828..4913
QY	1917	GACATTTTACGGGAGACATGCGCAATTTTGGATTTGCTGATGTTGATGCGGTAGT	1976	FT	intron	/tag= p /number= 3 4914..5012
DB	6741	GACATTTTACGGGAGACATGCGCAATTTTGGATTTGCTGATGTTGATGCGGTAGT	6800	FT	exon	/tag= q /number= 4 5013..5088
QY	1977	TTACTTGATGCTGCTCAACGATCTAATTCATGATGATTTATCTGATGCTGATCCATTGG	2036	FT	intron	/tag= r /number= 4 5089..5131
DB	6801	TTACTTGATGCTGCTCAACGATCTAATTCATGATGATTTATCTGATGCTGATCCATTGG	6860	FT	intron	/tag= s /number= 5 5132..5327
QY	2037	TGAAGATGTAAGTG 2050		FT	intron	/tag= t /number= 5 5328..5387
DB	6861	TGAAGATGTAAGTG 6874		FT	intron	/tag= u /number= 6 5388..5886
RESULT 3						
AAZ35393						
ID	AAZ35393	standard; DNA; 23449 BP.				
XX	AAZ35393;					
XX	27-MAR-2000	(first entry)				
XX	Maize	amylose-extender (Ae) gene encoding starch branching enzyme.				
XX	Starch	branching enzyme 1b; amylose-extender gene; Ae gene; maize; corn;				
XX	promoter;	expression control element; endospem; transgenic plant; ss.				
XX	Zea	mays.				
XX						

[illegible]



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XX 21-FEB-2000; 2000AU-00005742.
PR
XX (GSIR ) COMMONWEALTH SCI & IND RES ORG.
XX (GOOD-) GOODMAN FIELDER LTD.
PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
XX
PI Morell M, Rahman S;
XX
DR WPI; 2001-570635/64.
XX
XX Nucleic acids encoding wheat starch branching enzyme IIb, useful for
PT altering the amylose and amylopectin content of cereal plants, e.g. wheat
PT and barley.
XX
XX Example 1; Fig 1; 103pp; English.
XX
XX The present sequence encodes wheat starch branching enzyme 9, designated
CC Br1a. The specification describes Br1b. Br1b is a type II starch
CC branching enzyme (SBE). The Br1b nucleic acids may be used to
CC genetically transform cereal plants such as wheat or barley and for
CC altering their nutritional content by modulating the starch biosynthetic
CC pathway to vary levels of amylopectin and/or amylose produced in the
CC plant
XX
XX Sequence 2726 BP; 726 A; 564 C; 701 G; 735 T; 0 U; 0 Other;
SQ
XX
XX Query March 6.9%; Score 141; DB 5; Length 2726;
XX Best Local Similarity 72.2%; Pred. No.1.3e-22;
XX Matches 242; Conservative 0; Mismatches 5; Indels 88; Gaps 1.1;
XX
XX 1383 AGTCATTGTCGAATATATACCCCTTGACGGTTTGAATGGTTTGCATGACATGATACACAT 1442
Db 1168 AGTCATTATCAATATATATACCCCTTGACGGTTTGAATGGTTTGCATGACATGATACACAT 1227
XX
XX 1443 TACTTCCACGGTGTTCACACGGCCATCATTTGATGGGAAATTCGTCTATTCACATAT 1502
Qy 1228 TACTTCCACGGTGTTCACACGGCCATCATTTGATGGGAAATTCGTCTATTCACATAT 1287
XX
XX 1503 GGGAGTTGGGAAGTATGTAGCTCTGACTCTGTACACATATTTGGCTAACTGTCCTGT 1562
Qy 1288 GGGAGTTGGGAAG----- 1300
XX
XX 1563 AATCTGTTCTTACACATGTGATATTCTATTCTTAGCAGGATTTGAGANTCTTACTGTC 1622
Db 1301 -----TATTGAGATTTCTTACTGTC 1314
XX
XX 1623 AAACCCGAGATGTGCTGTGAAGAATATATAGTTTGATGATTTGGATTGGGGTAC 1682
Qy 1320 AAACCCGAGATGTGCTGTGAAGAATATATAGTTTGATGATTTGGATTGGGGTAC 1379
XX
XX 1683 CTCGATGATGTATCTCACCATGATTTACAAGTAA 1717
Qy 1380 CTCGATGATGTATCTCACCATGATTTACAAGTAA 1414
Db
XX
XX RESULT 6
XX AAAX34650/c
XX ID AAAX34650 standard; DNA; 11473 BP.
XX
XX AAAX34650;
XX
XX 17-OCT-2003 (revised)
XX 05-JUL-1999 (first entry)
XX
XX Starch branching enzyme II (SBE II) gene sequence.
XX
XX Starch biosynthetic pathway; cereal plant; enzyme; SBE; SSS; DBS; CBSS;
XX starch branching enzyme; starch soluble synthase; debranching enzyme;
XX endosperm; wheat; barley; granule-bound synthase; glutenin; starch;
XX grain softness protein I; bacterial isoamylase; glycogen synthase;
XX WSB1-1-D4 gene; ss.
XX

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XX	AAgiIops lauschni.
XX	FN
XX	PD
XX	25-MAR-1999.
XX	11-SEP-1998; 98WC-AU000743.
XX	PR 12-SEP-1997; 97AU-00009108.
XX	PR 20-MAR-1998; 98AU-00002509.
XX	(CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX	PA (AUSU ) UNIV AUSTRALIAN NAT.
XX	PA (GOOD-) GOODMAN FIELDER LTD.
XX	PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.
PI	Lt Z, Morell M, Rahman S;
XX	WT; 1999-229525/19.
XX	PT
XX	New isolated cereal plant enzyme genes used for, e.g. expression of
XX	antisense sequences of granule bound synthase.
PS	Claim 8; Page 75-81; 171pp; English.
XX	XX
CC	The invention relates to a novel enzyme of starch biosynthetic pathway in
CC	a cereal plant, where the enzyme is selected from starch branching enzyme
CC	(SBE) I, SBE II, starch soluble synthase (SSS) I, and debranching enzyme
CC	(DBE) with the proviso that the enzyme is not SSS I of rice, or SBE I of
CC	rice or maize. The methods and products can be used for targeting
CC	expression specifically to the endosperm of the seeds of cereal plants
CC	such as wheat or barley. They can be used for the expression of e.g.
CC	antisense sequences of granule-bound synthase (GBSS), SBE II, low mol.
CC	wt. glutenin, grain softness protein I, bacterial isomylase, bacterial
CC	glycogen synthase, and wheat high mol. wt. glutenin Bx1. They can be
CC	used for modifying the characteristics of starch produced by a plant. The
CC	present sequence represents the SBE II gene sequence. (Updated on 17-OCT-
CC	2003 to standardise OS field)
XX	XX
XX	Sequence 11473 BP; 3096 A; 2263 C; 2423 G; 3691 T; 0 U; 0 Other;
XX	Sequence 11473 BP; 3096 A; 2263 C; 2423 G; 3691 T; 0 U; 0 Other;
XX	Query Match 6.2%; Score 126.2; DB 2; Length 11473;
XX	Best Local Similarity 64.6%; Pred. No. 5.2e-19;
XX	Matches 188; Conservative 0; Mismatches 103; Indels 0; Gaps 0;
QY	911 ATGTTACTTCCTCCGTGTAATTCATTGACATATTAATTAAGTTCTTCATTGGCTCAA 970
DB	6028 ATCTATATTAATTTGATGTGTCCTCTGATCCAAATGATGAAGTTAGATTTCTCTAA 5969
QY	971 GTCAAACCTCTTAAAGTTTGAACCAAGCTCTATGGAATAATATATCAACATCAACACCA 1030
DB	5968 GTCAAACCTCTTAAATTTGACCAAGCTCTATGGAATAATGCTGTAATCTCAACATCA 5909
QY	1031 AATTAAGTTGATGAGTAAACAATTTTATTTTATTTATTAAGACATCTTGAATGTGT 1090
DB	5908 AAGATGTCATATTAATTAATAATTAATATGTTATCTGATCAAGATTAATTTGGTGTGT 5849
QY	1091 AGATATGACGACATTTTCTATAGACTGTGTAATAATAGAAAGTTTGACTTAGACCAA 1150
DB	5848 AGATGTTGATATATTTTCCAAATAGACTGTGCAACACTTAAGAAGTTTGACTTAGACCAA 5789
QY	1151 ATCTAAGAACTTCATCATTTTGGATCGAAGGACATCAATATATAGAT 1201
DB	5788 ATGAAGAACTTTAAGTAAATATGTTCAATGATTAACACAGGAAGTAAAT 5738
XX	RESULT 7
XX	AAH78338/C
XX	ID AAH78338 standard; cDNA; 11475 BP.
XX	AAH78338;
XX	26-NOV-2001 (first entry)

XX DE Nucleotide sequence of a starch branching enzyme designated F2.  
 XX KW wheat; starch branching enzyme; BE1b; SB2; transgenic plant;  
 XX KW starch biosynthetic pathway; amylopectin; F2; amylose; ss.  
 XX OS Aegilops tauschii.  
 XX PN WO200162934-A1.  
 XX PD 30-AUG-2001.  
 XX PF 21-FEB-2001; 2001MO-AU000175.  
 XX PR 21-FEB-2000; 2000AU-00005742.  
 XX PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
 XX PA (GOOD-) GOODMAN FIELDER LTD.  
 XX PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.  
 XX PI Morell W, Rahman S;  
 XX PI WPI; 2001-570635/64.  
 XX DR Nucleic acids encoding wheat starch branching enzyme IIB, useful for  
 XX PT altering the amylose and amylopectin content of cereal plants, e.g. wheat  
 XX PT and barley.  
 XX PS Example 1; Fig 2; 103pp; English.  
 XX CC The present sequence encodes a wheat starch branching enzyme of Aegilops  
 XX CC tauschii, designated F2. A. tauschii is likely to be the ancestral D  
 XX CC genome donor of wheat. Probes isolated from the present sequence were  
 XX CC used to identify type II starch branching enzymes (SBEs) in wheat,  
 XX CC especially BE1b. The BE1b nucleic acids may be used to genetically  
 XX CC transform cereal plants such as wheat or barley and for altering their  
 XX CC nutritional content by modulating the starch biosynthetic pathway to vary  
 XX CC levels of amylopectin and/or amylose produced in the plant  
 XX SQ Sequence 11475 BP; 3093 A; 2259 C; 2423 G; 3689 T; 0 U; 11 Other;  
 XX SQ  
 XX Query Match 6.2%; Score 126.2; DB 5; Length 11475;  
 XX Best Local Similarity 64.6%; Pred. No. 5.2e-19;  
 XX Matches 188; Conservative 0; Mismatches 103; Indels 0; Gaps 0;  
 QY 911 AAGTACTTCCCTGTTGAATTCATTGAACATATTAAGTTCTTCATTGCTCTAA 970  
 DB 6025 ATCTATATTTATTTGATGTTCCCTGATCCAAATTTGATGAAGTTCTGATTTGCTTA 5966  
 QY 971 GTCAACTTTCTTAAAGTTGACCAAGTCTATGSAATAATATCAACTTCAACACCA 1030  
 DB 5965 GTCAAACTTCTATATTTGACCAAGTCTATGSAATAATGCTGATATTCACACACCA 5906  
 QY 1031 AATTAATTTATGATGATTAACAATTTTATTTATTTATTAAGACATCTTGAATGTTGT 1090  
 DB 5905 ABAATGTCCTAATTAATTAATAAATTTATTCATGATCAAGTAAATTTGGTGTGT 5846  
 QY 1091 AGATATCAGACATTTTCTATAGACTTGTCAAAATATAGAAAGTTTGAAGACAA 1150  
 DB 5845 AGATGTTGATATTTTCCATAGACTTGTCAAAAGTTTGAAGTTTGAAGACAA 5786  
 QY 1151 ATCTAGAACTTCAATCAATTTGATCGAGGAAACATTAATAATATATGAT 1201  
 DB 5785 ATGAAGAACTTAAATATATGTTCAATGATTAACAGGAAAGTAAACAT 5735

XX DE Rice DNA sequence Seq ID523 related to grain filling.  
 XX KW plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;  
 XX KW carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;  
 XX KW tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;  
 XX KW wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;  
 XX KW gene; ds; plant.  
 XX OS Oryza sativa.  
 XX PN WO200300905-A2.  
 XX PD 03-JAN-2003.  
 XX PF 21-JUN-2002; 2002MO-IB002450.  
 XX PR 22-JUN-2001; 2001US-0300112P.  
 XX PR 26-SEP-2001; 2001US-0325277P.  
 XX PR 20-DEC-2001; 2001US-0342327P.  
 XX PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 XX PI Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;  
 XX PI Glazebrook J, Katagiri F, Kreps J, Provart N, Rieke D;  
 XX DR WPI; 2003-229341/22.  
 XX DR P-PsDB; ADC08219.  
 XX PS Claim 35; SEQ ID NO 523; 130pp; English.  
 XX CC This invention, in the area of plant biotechnology, relates to novel  
 XX CC polynucleotides comprising a nucleotide sequence encoding a protein which  
 XX CC is involved in or associated with the synthesis, metabolism or  
 XX CC degradation of carbohydrates in the plant grain and the expression of  
 XX CC which is up-regulated during grain filling. The plant is selected from  
 XX CC corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,  
 XX CC sugarbeet, wheat, and rice. The invention may be useful for the  
 XX CC improvement of protein, oil, starch, fibre and moisture content of the  
 XX CC cereal grains. In addition, carbohydrate levels may be modified to a more  
 XX CC desirable level using the present invention. The present sequence is a  
 XX CC DNA sequence encoding a rice protein of the invention. Note: The sequence  
 XX CC data for this patent did not form part of the printed specification, but  
 XX CC was obtained in electronic format directly from WIPO at  
 XX CC ftp.wipo.int/pub/publishedpct\_sequences.  
 XX SQ Sequence 2304 BP; 610 A; 457 C; 620 G; 617 T; 0 U; 0 Other;  
 XX SQ  
 XX Query Match 6.0%; Score 122.8; DB 9; Length 2304;  
 XX Best Local Similarity 91.5%; Pred. No. 2e-18;  
 XX Matches 130; Conservative 0; Mismatches 12; Indels 0; Gaps 0;  
 QY 1909 TTCTAGATGACATTTTACTGGAACCTATGCGAATATTTTGGATTTGCTACTGATGTTGAT 1968  
 DB 1384 TTACAGGTGACATTTTACTGGAACCTATGCGAATATTTTGGATTTGCTACTGATGTTGAT 1413  
 QY 1968 GGGAGATTTTACTGATGCTGTCACAGATCTAATTCATGAGCACTTATCCGTGATGCTGTA 2028  
 DB 1414 GGAGTATTTTACTGATGCTGTCGATGACATCTAATTCATGAGCACTTATCCGTGATGCTGTA 1473  
 QY 2029 TCCATTTGATGAGATGTAAGTG 2050  
 DB 1474 GCCATTTGATGAGATGTAAGTG 1495

RESULT 8  
 ADC08218 standard; DNA; 2304 BP.  
 AC ADC08218;  
 XX 18-DEC-2003 (first entry)

RESULT 9  
 ADA71289 standard; DNA; 2655 BP.  
 ID ADA71289

XX AD71289;  
AC 20-NOV-2003 (first entry)  
XX  
XX Rice gene, SEQ ID 4612.  
DE  
XX Plant, bacterial infection; fungal infection; viral infection; rice;  
KM gene; ds.  
XX  
XX Oryza sativa.  
OS  
XX WO2003000898-A1.  
PN  
XX 03-JAN-2003.  
PD  
XX 22-JUN-2001; 2001WO-IB001105.  
PF  
XX 22-JUN-2001; 2001WO-IB001105.  
PR  
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.  
PA  
XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;  
XX Katagiri F, Qian S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;  
XX WPI; 2003-175290/17.  
DR  
XX Identifying at least one gene involved in plant resistance or response to  
XX pathogenic infection for conferring resistance or tolerance to a plant to  
XX bacterial, fungal or viral infection by determining or detecting plant  
XX gene expression.  
PT  
XX  
PS Claim 6; SEQ ID NO 4612; 899p; English.  
XX  
XX The present invention relates to a method (M1) for identifying genes  
XX involved in plant resistance or response to pathogenic infection. M1  
XX comprises identifying a gene whose expression is significantly altered in  
XX the incompatible interaction of plant gene expression relative to  
XX expression of the gene in an uninfected plant, in a mutant plant that  
XX does not express a gene associated with response to pathogenic infection,  
XX or in a corresponding incompatible or compatible interaction. (M1) is  
XX useful for conferring resistance to resistance or tolerance to a plant to  
XX bacterial, fungal or viral infection. The present sequence was used to  
XX illustrate the invention.  
XX  
XX Sequence 2655 BP; 714 A; 529 C; 680 G; 732 T; 0 U; 0 Other;  
SQ  
XX  
XX Query Match 6.0%; Score 122.8; DB 7; Length 2655;  
XX Best Local Similarity 91.5%; Pred. No. 2.1e-18;  
XX Matches 130; Conservative 0; Mismatches 12; Indels 0; Gaps 0;  
XX  
XX 1909 TTCTAGATGACATTACTGGAACATATTTGGATTGCTACTGATGTTGAT 1968  
XX |||||  
XX 1573 TTACAGGAGGATTTACTGGCACTATGCGAATATTTGGATTGCTACTGATGTTGAT 1632  
XX |||||  
XX 1969 GCGGTAGTTTACTGATGCTGCTCAAGCATCTAATTCATGACTTTATCTGATGCTGA 2028  
XX |||||  
XX 1633 GCACTAGTTTACTGATGCTGCTGTAACGATCTAATTCATGAGCTTATCTGAGGCTGA 1692  
XX |||||  
XX 2029 TCCATTGGTGAAGATGTAAGTG 2050  
XX |||||  
XX 1693 GCCATTGGTGAAGATGTCAGCG 1714  
XX |||||  
XX  
XX RESULT 10  
XX ID AAV05639 standard; cDNA to mRNA; 3015 BP.  
XX  
XX AAV05639;  
AC  
XX 25-MAR-2003 (revised)  
DT  
XX 01-MAY-1998 (first entry)  
XX

DE Rice type IV starch branching enzyme cDNA.  
XX  
XX Rice; type IV starch branching enzyme; amylopectin synthesis; ds.  
XX  
XX Oryza sativa.  
OS  
XX  
XX Key Location/Qualifiers  
XX CDS 129..2654  
XX /\*tag= a  
XX FT sig\_peptide 129..287  
XX /\*tag= b  
XX FT mat\_peptide 288..2651  
XX /\*tag= c  
XX FT /\*product= "type\_IV\_starch\_branching\_enzyme"  
XX  
XX JP10004970-A.  
XX  
XX 13-JAN-1998.  
XX  
XX 24-JUN-1996; 96JP-00162983.  
XX  
XX 24-JUN-1996; 96JP-00162983.  
XX  
XX PR 24-JUN-1996; 96JP-00162983.  
XX  
XX (MITS-) MITSUI TOYOSAI SHOKUBUTSU BIO KENKYUSHO.  
XX (MITK ) MITSUI TOYOSAI CHEM INC.  
XX  
XX WPI; 1998-133625/13.  
XX  
XX P-PSDB; AAW41763.  
XX  
XX Rice starch branching enzyme gene - synthesises amylopectin to yield high  
XX quality starch.  
XX  
XX  
XX Claim 4; Page 5-8, 13pp; Japanese.  
XX  
XX The present sequence encodes the rice type IV starch branching enzyme,  
XX which has the ability to synthesise amylopectin. The quality of starch is  
XX improved by the use of the protein. (Updated on 25-MAR-2003 to correct PA  
XX field.)  
XX  
XX Sequence 3015 BP; 796 A; 606 C; 819 G; 794 T; 0 U; 0 Other;  
SQ  
XX  
XX Query Match 6.0%; Score 122.8; DB 2; Length 3015;  
XX Best Local Similarity 91.5%; Pred. No. 2.2e-18;  
XX Matches 130; Conservative 0; Mismatches 12; Indels 0; Gaps 0;  
XX  
XX 1909 TTCTAGATGACATTTACTGGAACATATTTGGATTGCTACTGATGTTGAT 1968  
XX |||||  
XX 1626 TTACAGGTGACATTTACTGGAACATATTTGGATTGCTACTGATGTTGAT 1685  
XX |||||  
XX 1969 GCGGTAGTTTACTGATGCTGCTCAAGCATCTAATTCATGACTTTATCTGATGCTGA 2028  
XX |||||  
XX 1686 GCGGTAGTTTACTGATGCTGCTGTAACGATCTAATTCATGAGCTTATCTGAGGCTGA 1745  
XX |||||  
XX 2029 TCCATTGGTGAAGATGTAAGTG 2050  
XX |||||  
XX 1746 GCCATTGGTGAAGATGTCAGCG 1767  
XX |||||  
XX  
XX RESULT 11  
XX ID ADC07807 standard; DNA; 2307 BP.  
XX  
XX ADC07807;  
AC  
XX  
XX 18-DEC-2003 (first entry)  
DT  
XX  
XX Rice DNA sequence seg ID73 related to grain filling.  
XX  
XX Plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;  
XX carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;  
XX tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarcane;  
XX wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;  
XX gene; ds. plant  
XX



XX Oryza sativa.  
OS  
PN MO2003000905-A2.  
XX  
PD 03-JAN-2003.  
XX  
PF 21-JUN-2002; 2002MO-IB002450.  
XX  
PR 22-JUN-2001; 2001US-0300112P.  
PR 26-SEP-2001; 2001US-0325277P.  
PR 20-DEC-2001; 2001US-0342327P.  
XX  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX  
PI Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;  
PI Glazebrook J, Katagiri F, Kreps J, Provart N, Ricke D;  
XX  
DR MPI; 2003-229341/22.  
XX  
DR P-PSDB; ADC07808.  
XX  
PT New plant genes encoding polypeptides having an activity involved in or  
PT associated with the synthesis, metabolism or degradation of carbohydrates  
PT in the plant grain useful in generating plants having improved  
PT nutritional properties.  
PS  
PS Claim 2; SEQ ID NO 73; 130pp; English.  
XX  
CC This invention, in the area of plant biotechnology, relates to novel  
CC polynucleotides comprising a nucleotide sequence encoding a protein which  
CC is involved in or associated with the synthesis, metabolism or  
CC degradation of carbohydrates in the plant grain and the expression of  
CC which is up-regulated during grain filling. The plant is selected from  
CC corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,  
CC sugarcane, wheat, and rice. The invention may be useful for the  
CC improvement of protein, oil, starch, fibre and moisture content of the  
CC cereal grains. In addition, carbohydrate levels may be modified to a more  
CC desirable level using the present invention. The present sequence is a  
CC DNA sequence encoding a rice protein of the invention. Note: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/publishedpc\_sequences.  
CC  
SQ Sequence 2307 BP; 608 A; 465 C; 620 G; 614 T; 0 U; 0 Other;  
Query Match 5.8%; Score 119.2; DB 9; Length 2307;  
Best Local Similarity 85.3%; Pred. No. 1.4e-17;  
Matches 133; Conservative 0; Mismatches 23; Indels 0; Gaps 0;  
QY 1895 AAGTTGTTCTGTTCTAGATGACATTGAGGAACTATGCGAATATTTGGATTG 1954  
Db 1279 ATGTAATCTATCATCTGTTTACACATTCTGGAATTAAGCGAATATTTGGATTG 1338  
QY 1955 CTACTGATGTTGATGCGGTAATTTACTTGTATGCTGTCACAGATCTAATTCATGGACTTT 2014  
Db 1339 CTAAGTATGTTGATGAGTATGATTTACTTGTATGCTGTCACAGATCTAATTCATGGACTTT 1398  
QY 2015 ATCCTGATGCTGATTCATTCATTCGTAAGATGTAAGT 2050  
Db 1399 ATCCTGAGGCTGTAAGCCATTGTAAGATGTAAGTCAAGC 1434  
RESULT 12  
AAT69737  
ID AAT69737 standard; DNA; 2087 BP.  
XX  
XX AAT69737;  
AC  
XX  
XX 10-SEP-1997 (first entry)  
DT  
XX  
XX Corn starch branching enzyme IIb gene fragment in pBB96.  
DE  
XX  
XX Starch branching enzyme IIb; SBEIIb; corn; maize; antisense; amylopectin;

KM transgenic plant; pBB96; ss.  
XX  
XX Zea mays.  
OS  
XX  
PN MO9722703-A2.  
XX  
PD 26-JUN-1997.  
XX  
PF 12-DEC-1996; 96WO-US019678.  
XX  
PR 20-DEC-1995; 95US-0009113P.  
XX  
PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
XX  
PI Hubbard NL, Klein TW, Broglie KE;  
XX  
DR MPI; 1997-341694/31.  
XX  
XX Transgenic corn in which grain derived starch fine structure is  
PT controlled - specifically branch chain distribution of amylopectin,  
PT useful in preparation of thickened foodstuff.  
PS  
PS Example 4; Page 56-57; 92pp; English.  
XX  
CC A cDNA insert (AAT69737) in plasmid pBB96 comprises a 2.09 kb fragment of  
CC corn starch branching enzyme IIb (SBEIIb) cDNA (see also AAT69729),  
CC starting at the initiating ATG codon of the coding region and terminating  
CC 312 bp 5' of the translation termination codon. It was obt'd. by site-  
CC specific mutagenesis of the SBEIIb gene in plasmid pBB240 to generate an  
CC NcoI site at the ATG start site, and EcoRI digestion of the mutagenised  
CC plasmid. The 2.09 kb fragment was inserted, in sense orientation, between  
CC the zein promoter and 3' regions in vector pML103 to produce pBB96. Co-  
CC suppression and antisense techniques can be used to inhibit SBEIIb in  
CC transgenic plants and thereby alter starch properties  
XX  
SQ Sequence 2087 BP; 565 A; 396 C; 553 G; 573 T; 0 U; 0 Other;  
Query Match 5.4%; Score 110.6; DB 2; Length 2087;  
Best Local Similarity 79.4%; Pred. No. 1.3e-15;  
Matches 131; Conservative 0; Mismatches 34; Indels 0; Gaps 0;  
QY 1383 AGTCATTCGTCGAATATATCCCTTGACGGTTGAAATGCTTTCGATGSCACTGATACAT 1442  
Db 1138 AGTCATTCGTCGAATATATCCCTTGACGGTTGAAATGCTTTCGATGSCACTGATACAT 1197  
QY 1443 TACTTCACAGTGTGTCACGCGCCATTCATTTGGATGCGATTCCTGCTATTCACATAT 1502  
Db 1198 TACTTCACAGTGTGTCACGCGCCATTCATTCATTTGGATGCGATTCCTGCTATTCAT 1257  
QY 1503 GGAAGTGGGAAGATATGATGCTGACTGCTGTCACCAATATTTGG 1547  
Db 1258 GGAAGTGGGAAGTATTTAGATTTCTCTCTCCAAATGCTGATGG 1302  
RESULT 13  
AAT69736/c  
ID AAT69736 standard; DNA; 2165 BP.  
XX  
XX AAT69736;  
AC  
XX  
XX 10-SEP-1997 (first entry)  
DT  
XX  
XX Corn starch branching enzyme IIb gene fragment in pBB45.  
DE  
XX  
XX Starch branching enzyme IIb; SBEIIb; corn; maize; antisense; amylopectin;  
KM transgenic plant; pBB45; ss.  
XX  
XX Zea mays.  
OS  
XX  
XX MO9722703-A2.  
PN  
XX  
XX 26-JUN-1997.  
PD





GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 10, 2004, 03:15:35 ; Search time 145.768 seconds  
(without alignments)  
7804.525 Million cell updates/sec

Title: US-09-508-377-10\_COPY\_4818\_6867

Perfect score: 2050

Sequence: 1 ccgaagaattcatcgc.....catgtggaagatgtaagt 2050

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_NA:\*

- 1: /cgn2\_6/ptodata/2/ina/5A.COMB.seq:\*
- 2: /cgn2\_6/ptodata/2/ina/5B.COMB.seq:\*
- 3: /cgn2\_6/ptodata/2/ina/6A.COMB.seq:\*
- 4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq:\*
- 5: /cgn2\_6/ptodata/2/ina/PTCUS.COMB.seq:\*
- 6: /cgn2\_6/ptodata/2/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	144.2	7.0	2853	4	US-09-609-040-3 Sequence 3, Appl1
2	122.2	6.0	2446	4	US-09-731-166-9 Sequence 9, Appl1
3	110.6	5.4	2087	4	US-09-257-894-9 Sequence 9, Appl1
4	110.6	5.4	2165	4	US-09-257-894-8 Sequence 8, Appl1
5	110.6	5.4	2665	4	US-09-257-894-1 Sequence 1, Appl1
6	110.6	5.4	2720	4	US-09-731-166-11 Sequence 11, Appl1
7	110.6	5.4	2725	3	US-08-941-445A-14 Sequence 14, Appl1
8	94	4.6	1393	3	US-09-087-277-3 Sequence 3, Appl1
9	94	4.6	1393	4	US-09-658-499-3 Sequence 3, Appl1
10	94	4.6	3074	4	US-09-087-277-1 Sequence 1, Appl1
11	94	4.6	3074	4	US-09-658-499-1 Sequence 1, Appl1
12	93.6	4.6	303	4	US-09-313-294A-6200 Sequence 6200, Ap
13	74.4	3.6	10322	3	US-09-330-330-3 Sequence 3, Appl1
14	71.2	3.5	1809	4	US-09-257-894-25 Sequence 25, Appl1
15	71.2	3.5	1865	4	US-09-257-894-20 Sequence 20, Appl1
16	71.2	3.5	2470	4	US-09-731-166-13 Sequence 13, Appl1
17	71.2	3.5	2487	4	US-09-257-894-19 Sequence 19, Appl1
18	71.2	3.5	2565	4	US-09-257-894-24 Sequence 24, Appl1
19	71.2	3.5	2763	3	US-08-941-445A-16 Sequence 16, Appl1
20	71.2	3.5	2772	4	US-09-257-894-12 Sequence 12, Appl1
21	67.8	3.3	2909	3	US-08-104-158-1 Sequence 1, Appl1
22	67.8	3.3	2909	4	US-09-609-040-1 Sequence 1, Appl1
23	67.8	3.3	3128	3	US-08-716-449-1 Sequence 1, Appl1
24	67.8	3.3	3128	4	US-09-367-895-29 Sequence 29, Appl1
25	67.8	3.3	11478	3	US-08-981-803-29 Sequence 29, Appl1

28	56.6	2.8	5402	4	US-09-221-017B-194 Sequence 194, App
29	54	2.6	807	1	US-08-165-315D-1 Sequence 1, Appl1
30	54	2.6	807	3	US-08-702-609A-2 Sequence 2, Appl1
31	54	2.6	846	1	US-08-165-315D-2 Sequence 2, Appl1
32	54	2.6	1327	1	US-08-165-315D-3 Sequence 3, Appl1
33	51.4	2.5	7218	1	US-08-232-463-14 Sequence 14, Appl1
34	49.6	2.4	1026	3	US-09-105-350-13 Sequence 13, Appl1
35	49.6	2.4	2169	3	US-09-105-390-5 Sequence 5, Appl1
36	48.8	2.4	6733	3	US-09-124-541-2 Sequence 2, Appl1
37	48.8	2.4	6733	4	US-09-663-336-2 Sequence 2, Appl1
38	47	2.3	658	3	US-08-998-416-595 Sequence 595, App
39	44.4	2.2	640681	4	US-09-790-968-1 Sequence 1, Appl1
40	44.2	2.2	4818	3	US-08-817-926-27 Sequence 27, Appl1
41	43.8	2.1	832	4	US-09-621-976-2813 Sequence 2813, Ap
42	43.8	2.1	832	4	US-09-621-976-2813 Sequence 2813, Ap
43	42.2	2.1	1026	3	US-09-105-350-13 Sequence 13, Appl1
44	42.2	2.1	2169	3	US-09-105-390-5 Sequence 5, Appl1
45	41.8	2.0	9347	4	US-10-204-708-35 Sequence 35, Appl1

ALIGNMENTS

RESULT 1									
US-09-609-040-3									
; Sequence 3, Application US/09609040									
; Patent No. 6570066									
; GENERAL INFORMATION:									
; APPLICANT: Wilmutizer, et al.									
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING ENZYMES THAT ALTER THE CARBOHYDRAT									
; FILE REFERENCE: 514413-3515.1									
; CURRENT APPLICATION NUMBER: US/09/609,040									
; PRIOR APPLICATION NUMBER: PCT/EP92/00302									
; PRIOR FILING DATE: 1992-02-11									
; NUMBER OF SEQ ID NOS: 4									
; SOFTWARE: PatentIn version 3.0									
; SEQ ID NO 3									
; LENGTH: 2853									
; TYPE: DNA									
; ORGANISM: Triticum aestivum									
; FEATURE:									
; NAME/KEY: CDS									
; LOCATION: (313)..(2499)									
; OTHER INFORMATION: BRANCHING ENZYME									
US-09-609-040-3									
Query Match									
Best local Similarity 72.8%; Pred. No. 1.9e-28;									
Matches 244; Conservative 0; Mismatches 3; Indels 88; Gaps 1;									
QY	1383	AGTCATTCGTC	AAATTAATACCCTTGACCGGTTG	AAATGTTTGATG	GGCACTATACACAT	1442			
DB	1240	AGTCATTCGTC	AAATTAATACCCTTGACCGGTTG	AAATGTTTGATG	GGCACTATACACAT	1299			
QY	1443	TACTTCACAGG	TGTCACGGCGGCATCAT	TGATGATG	GGATTCGCTATCAACTAT	1502			
DB	1300	TACTTCACAGG	TGTCACGGCGGCATCAT	TGATGATG	GGATTCGCTATCAACTAT	1359			
QY	1503	GGGAGTGGAG	AGATGATGACCTG	CACTTCGTG	CACCATATTTGGCTA	CTGCTGTT	1562		
DB	1360	GGGAGTGGAG	AGATGATGACCTG	CACTTCGTG	CACCATATTTGGCTA	CTGCTGTT	1371		
QY	1563	AAATCTGTTT	TACACATGTTGAT	TATCTATCTTATG	CAGGATTTGAGATTTCTT	ATCTGTC	1622		
DB	1372	AAATCTGTTT	TACACATGTTGAT	TATCTATCTTATG	CAGGATTTGAGATTTCTT	ATCTGTC	1391		
QY	1623	AAACGAGATG	GGGCTTGAGATAT	AAATTTGATGATTTG	ATTTGATG	GGGATGAC	1682		
DB	1392	AAACGAGATG	GGGCTTGAGATAT	AAATTTGATGATTTG	ATTTGATG	GGGATGAC	1451		

Mon Apr 12 10:24:24 2004

us-09-508-377-10\_copy\_4818\_6867.rn1

Page 2

DB 1452 CTCGATGATGTATCTCCATGATGATTAACAAATCA 1486

RESULT 2  
US-09-731-166-9

Sequence 9, Application US/09731166  
Patent No. 6639126  
GENERAL INFORMATION:  
APPLICANT: Sewalt, Vincent J. H.  
APPLICANT: Singletary, George W.  
TITLE OF INVENTION: Production of Modified Polysaccharides  
FILE REFERENCE: 35718/206348  
CURRENT APPLICATION NUMBER: US/09/731,166  
CURRENT FILING DATE: 2000-12-06  
PRIOR APPLICATION NUMBER: 60/169,993  
PRIOR FILING DATE: 1999-12-06  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 9  
LENGTH: 2446  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (0)...(0)  
OTHER INFORMATION: SBE11a  
NAME/KEY: CDS  
LOCATION: (2)...(2446)  
US-09-731-166-9

Query Match 6.0%; Score 122.2; DB 4; Length 2446;  
Best Local Similarity 88.1%; Pred. No. 1.2e-22;  
Matches 133; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

DB 1383 AGTCATTCGCAATATATACCCCTGACGGTTGTAAGTTCGATGGACATGATACAT 1442  
1172 AGTCATTCGCAATATATACCCCTGACGGTTGTAAGTTCGATGGACATGATACAT 1231  
QY 1443 TACTTCCAGGTTGTCACGCGCCATCATTCGATGGATTCCTCTATTCATCACTAT 1502  
DB 1232 TACTTCCAGGTTGTCACGCGCCATCATTCGATGGATTCCTCTATTCATCACTAT 1291  
QY 1503 GGGAGTTGGGAAGTATGATGCTTGACTTCT 1533  
DB 1292 GGGAGTTGGGAAGTATGATGCTTGACTTCT 1322

RESULT 3  
US-09-257-894-9

Sequence 9, Application US/09257894  
Patent No. 6376749  
GENERAL INFORMATION:  
APPLICANT: Broglie, Karen E.  
APPLICANT: Klein, Theodore M.  
APPLICANT: Hubbard, Natalie L.  
APPLICANT: Lightner, Jonathan E.  
TITLE OF INVENTION: No. 6376749el Starches via Modification of  
TITLE OF INVENTION: Expression of Starch Biosynthesis  
TITLE OF INVENTION: Enzyme Genes  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: E. I. du Pont de Nemours and Company  
STREET: 1007 Market Street  
CITY: Wilmington  
STATE: Delaware  
COUNTRY: USA  
ZIP: 19898

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Microsoft Windows 95

SOFTWARE: Version 7.0A  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/257,894  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/091,052  
FILING DATE: JUNE 10, 1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Majarian, William R.  
REGISTRATION NUMBER: 41,173  
REFERENCE/DOCKET NUMBER: BB-1066-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 302-992-4926  
TELEX: 302-773-0164  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2087 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-257-894-9

Query Match 5.4%; Score 110.6; DB 4; Length 2087;  
Best Local Similarity 79.4%; Pred. No. 1.4e-19;  
Matches 131; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

DB 1383 AGTCATTCGCAATATATACCCCTGACGGTTGTAAGTTCGATGGACATGATACAT 1442  
1138 AGTCATTCGCAATATATACCCCTGACGGTTGTAAGTTCGATGGACATGATACAT 1197  
QY 1443 TACTTCCAGGTTGTCACGCGCCATCATTCGATGGATTCCTCTATTCATCACTAT 1502  
DB 1198 TACTTCCAGGTTGTCACGCGCCATCATTCGATGGATTCCTCTATTCATCACTAT 1257  
QY 1503 GGGAGTTGGGAAGTATGATGCTTGACTTCTGACCATATTTGG 1547  
DB 1258 GGGAGTTGGGAAGTATGATGCTTGACTTCTGACCATATTTGG 1302

RESULT 4  
US-09-257-894-8/c

Sequence 8, Application US/09257894  
Patent No. 6376749  
GENERAL INFORMATION:  
APPLICANT: Broglie, Karen E.  
APPLICANT: Klein, Theodore M.  
APPLICANT: Hubbard, Natalie L.  
APPLICANT: Lightner, Jonathan E.  
TITLE OF INVENTION: No. 6376749el Starches via Modification of  
TITLE OF INVENTION: Expression of Starch Biosynthesis  
TITLE OF INVENTION: Enzyme Genes  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: E. I. du Pont de Nemours and Company  
STREET: 1007 Market Street  
CITY: Wilmington  
STATE: Delaware  
COUNTRY: USA  
ZIP: 19898

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Microsoft Windows 95  
SOFTWARE: Version 7.0A  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/257,894  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/091,052  
FILING DATE: JUNE 10, 1998

```
ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1066-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2165 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-257-894-8

Query Match
Best Local Similarity 5.4%; Score 110.6; DB 4; Length 2165;
Matches 131; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1383 AGTCATTGCTCAAAATATATACCCCTTGACGGTTTGATGTTTCGATGCGACTGATACAT 1442
DB 950 AGTCATGCGCTCAAGTAATATCTGATGGTGTGATGTTGATGCTGACATGATACAT 891
QY 1443 TACTTCACAGGTGGTCCACGCGGCATCATTTGATGGGATTCCTGCTATTCACTAT 1502
DB 890 TACTTCACAGGTGGTCCACGCGGCATCATTTGATGGGATTCCTGCTATTCACTAT 831
QY 1503 GGGAGTTGGAGATATAGTCTGACTGATCTGTGTCACCATATTGG 1547
DB 830 GGGAGCTGGAGATTTAAGATTCTTCTCTCCCAATGCTATATGG 786

RESULT 5
US-09-257-894-1
Sequence 1, Application US/09257894
Patent No. 6376749
GENERAL INFORMATION:
APPLICANT: Broglie, Karen E.
APPLICANT: Klein, Theodore M.
APPLICANT: Hubbard, Natalie L.
APPLICANT: Lightner, Jonathan E.
TITLE OF INVENTION: No. 6376749el Starches via Modification of
TITLE OF INVENTION: Expression of Starch Biosynthesis
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESS: E. I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Version 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/257,894
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/091,052
FILING DATE: JUNE 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1066-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164
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SEQUENCE CHARACTERISTICS:
LENGTH: 2665 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 79..2476
US-09-257-894-1

Query Match
Best Local Similarity 5.4%; Score 110.6; DB 4; Length 2665;
Matches 131; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1383 AGTCATTGCTCAAAATATATACCCCTTGACGGTTTGATGTTTCGATGCGACTGATACAT 1442
DB 1216 AGTCATGCGCTCAAGTAATATCTGATGGTGTGATGTTGATGCTGACATGATACAT 1275
QY 1443 TACTTCACAGGTGGTCCACGCGGCATCATTTGATGGGATTCCTGCTATTCACTAT 1502
DB 1276 TACTTCACAGGTGGTCCACGCGGCATCATTTGATGGGATTCCTGCTATTCACTAT 1335
QY 1503 GGGAGTTGGAGATATAGTCTGACTGATCTGTGTCACCATATTGG 1547
DB 1336 GGGAGCTGGAGATTTAAGATTCTTCTCTCCCAATGCTATATGG 1380

RESULT 6
US-09-731-166-11
Sequence 11, Application US/09731166
Patent No. 6639126
GENERAL INFORMATION:
APPLICANT: Sewalt, Vincent J. H.
APPLICANT: Singletary, George W.
TITLE OF INVENTION: Production of Modified Polysaccharides
FILE REFERENCE: 35718/206348
CURRENT APPLICATION NUMBER: US/09/731,166
CURRENT FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: 60/169,993
PRIOR FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 2720
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)..(0)
OTHER INFORMATION: SBRlib
OTHER INFORMATION: Genbank Accession No. 6639126 AF072725
NAME/KEY: CDS
LOCATION: (101)..(2500)
US-09-731-166-11

Query Match
Best Local Similarity 5.4%; Score 110.6; DB 4; Length 2720;
Matches 131; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1383 AGTCATTGCTCAAAATATATACCCCTTGACGGTTTGATGTTTCGATGCGACTGATACAT 1442
DB 1238 AGTCATGCGCTCAAGTAATATCTGATGGTGTGATGTTGATGCTGACATGATACAT 1297
QY 1443 TACTTCACAGGTGGTCCACGCGGCATCATTTGATGGGATTCCTGCTATTCACTAT 1502
DB 1298 TACTTCACAGGTGGTCCACGCGGCATCATTTGATGGGATTCCTGCTATTCACTAT 1357
QY 1503 GGGAGTTGGAGATATAGTCTGACTGATCTGTGTCACCATATTGG 1547
DB 1358 GGGAGCTGGAGATTTAAGATTCTTCTCTCCCAATGCTATATGG 1402
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RESULT 7  
US-08-941-445A-14  
; Sequence 14, Application US/08941445A  
; Patent No. 6107060  
; GENERAL INFORMATION:  
; APPLICANT: Keeling, Peter  
; APPLICANT: Guan, Haining  
; TITLE OF INVENTION: Starch Encapsulation  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
; STREET: 5370 Manhattan Circle  
; CITY: Boulder  
; STATE: CO  
; COUNTRY: US  
; ZIP: 80303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/941,445A  
; FILING DATE: 30-SEP-1997  
; CLASSIFICATION: 800  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 60/026,855  
; FILING DATE: 30-SEP-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winner, Ellen P  
; REGISTRATION NUMBER: 28,547  
; REFERENCE/DOCKET NUMBER: 89-97  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (303) 499-8080  
; TELEFAX: (303) 499-8089  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2725 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: mRNA  
; HYPOTHEICAL: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: 91..264  
; FEATURE:  
; NAME/KEY: mat\_peptide  
; LOCATION: 265..2487  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 91..2490  
US-08-941-445A-14  
Query Match 5.4%; Score 110.6; DB 3; Length 2725;  
Best Local Similarity 79.4%; Pred. No. 1.6e-19;  
Matches 131; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1383 AGTCATTCGTCGAATATATACCCCTTGAGCGTTGTAATGGTTCCATGGCAGCTGATACACAT 1442  
DB 1228 AGTCAGCGCGTCAGATATATCTCGAGGCGTTGATGGTTGATGATACAGATACACAT 1287  
QY 1443 TACTTCACAGGTGTCACACCGGCACATCATGATGTGGATTCCTGCTATTCACATAT 1502  
DB 1288 TACTTTCACAGTGTGTCACAGCGGCACATCATGATGTGGATTCCTGCTATTCACATAT 1347  
QY 1503 GGGAGTTGGAGAGTATGTAGCTTGACTTCTGTCACATATTTGG 1547  
DB 1348 GGGAACTGGGAGATTTAAGATTTCCTCTCCAACTGATGATG 1392

RESULT 8  
US-09-087-277-3  
; Sequence 3, Application US/09087277B  
; Patent No. 6169226  
; GENERAL INFORMATION:  
; APPLICANT: EK, Bo  
; APPLICANT: KHOSNODI, Jamsheed  
; APPLICANT: LARSSON, Claas-Tomas  
; APPLICANT: LARSSON, Hakar  
; APPLICANT: PASK, Lars  
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO  
; FILE REFERENCE: 003300-486  
; CURRENT APPLICATION NUMBER: US/09/087,277B  
; CURRENT FILING DATE: 1998-05-29  
; EARLIER APPLICATION NUMBER: PCT/SE96/01558  
; EARLIER FILING DATE: 1996-11-28  
; EARLIER APPLICATION NUMBER: SE 9504272-7  
; EARLIER FILING DATE: 1995-11-29  
; EARLIER APPLICATION NUMBER: SE 9601506-0  
; EARLIER FILING DATE: 1996-04-19  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 1393  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism:beil gene fragment  
; OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum  
; OTHER INFORMATION: (potato)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (2)..(1393)  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (424)..(1150)  
; OTHER INFORMATION: Nucleotides 424, 891 and 1150 are n wherein n = A,  
; OTHER INFORMATION: C, G or T.  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (422)..(424)  
; OTHER INFORMATION: Amino acid 141 is Xaa wherein Xaa = Thr.  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (890)..(892)  
; OTHER INFORMATION: Amino acid 297 is Xaa wherein Xaa = Tyr, Ser, Cys  
; OTHER INFORMATION: or Phe.  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1148)..(1150)  
; OTHER INFORMATION: Amino acid 383 is Xaa wherein Xaa = Pro.  
US-09-087-277-3  
Query Match 4.6%; Score 94; DB 3; Length 1393;  
Best Local Similarity 78.9%; Pred. No. 2.9e-15;  
Matches 112; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1909 TTCTAGATGACATTTACTGCGGAGCACTATGCGGAATATTTGATTTGCTACTGATGTGAT 1968  
DB 734 TTATGGGTGGGATTCACCTGGGAGCACTATGCGGAATATTTGATTTGCTACTGATGTGAT 793  
QY 1969 GCGGTAGTTTACTGATGCTGTGTCACGATCTTAATTCATGAGCACTTATCTGATGCTGTA 2028  
DB 794 GCTGTGTGTATCTGATGCTGTGTCACGATCTTATTCATGAGCACTTATTCATGAGCAAT 853  
QY 2029 TCCATTGCTGAAGATGATG 2050  
DB 854 ACCATTGCTGAAGATGTTAGCG 875

RESULT 9  
US-09-658-499-3  
; Sequence 3, Application US/09658499

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/ Patent No. 6469231
/ GENERAL INFORMATION:
/ APPLICANT: EK, Bo
/ APPLICANT: KHOSNODI, Jamshid
/ APPLICANT: LARSSON, Clas-Tomas
/ APPLICANT: LARSSON, Hakan
/ APPLICANT: RASK, Lars
/ TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
/ FILE REFERENCE: 003300-486
/ CURRENT APPLICATION NUMBER: US/09/658,499
/ CURRENT FILING DATE: 2000-09-08
/ PRIOR APPLICATION NUMBER: 09/087,277
/ PRIOR FILING DATE: 1998-05-29
/ PRIOR APPLICATION NUMBER: PCT/SE96/01558
/ PRIOR FILING DATE: 1996-11-28
/ PRIOR APPLICATION NUMBER: SE 9504272-7
/ PRIOR FILING DATE: 1995-11-29
/ PRIOR APPLICATION NUMBER: SE 9601506-0
/ PRIOR FILING DATE: 1996-04-19
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 3
/ LENGTH: 1393
/ TYPE: DNA
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: Description of Unknown Organism:beli gene fragment
/ OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
/ OTHER INFORMATION: (potato)
/ NAME/KEY: CDS
/ LOCATION: (2)..(1393)
/ NAME/KEY: misc_feature
/ LOCATION: (424)..(1150)
/ OTHER INFORMATION: Nucleotides 424, 891 and 1150 are n wherein n = A,
/ OTHER INFORMATION: C, G or T.
/ NAME/KEY: misc_feature
/ LOCATION: (422)..(424)
/ OTHER INFORMATION: Amino acid 141 is Xaa wherein Xaa = Thr.
/ NAME/KEY: misc_feature
/ LOCATION: (1890)..(1892)
/ OTHER INFORMATION: Amino acid 297 is Xaa wherein Xaa = Tyr, Ser, Cys
/ OTHER INFORMATION: or Phe.
/ NAME/KEY: misc_feature
/ LOCATION: (1148)..(1150)
/ OTHER INFORMATION: Amino acid 383 is Xaa wherein Xaa = Pro.
/ US-09-658-499-3
/
/ Query Match 4.6%; Score 94; DB 4; Length 1393;
/ Best Local Similarity 78.9%; Pred. No. 2,9e-15;
/ Matches 112; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
/
/ QY 1909 TTCTAGATGACATTACTGCGAAGTATGCGAATATTTGGATTGCTACTGATGTTGAT 1968
/ DB 734 TTATCGGTGGATTCTCTGGAACTACGAGAACTACTTGATCGGAAGTGAATGATGAT 793
/
/ QY 1969 GCGGTAGTTACTTGATGCTGTCACGATCTAATTCAGGACTTATTCGTGATGCTGA 2028
/ DB 794 GCTGTGTATCTGATGCTGTCACGATCTTATTCATGGGCTTTCCAGATGCAATT 853
/
/ QY 2029 TCCATTGTTGAAGATGTAAGTG 2050
/ DB 854 ACCATTGTGAAGATGTTAGCG 875
/
/ RESULT 10
/ US-09-087-277-1
/ Sequence 1, Application US/09087277B
/ Patent No. 6169226
/ GENERAL INFORMATION:
/ APPLICANT: EK, Bo
/ APPLICANT: KHOSNODI, Jamshid
/ APPLICANT: LARSSON, Clas-Tomas
/ APPLICANT: LARSSON, Hakan
```

```
/ APPLICANT: RASK, Lars
/ TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
/ FILE REFERENCE: 003300-486
/ CURRENT APPLICATION NUMBER: US/09/087,277B
/ CURRENT FILING DATE: 1998-05-29
/ EARLIER APPLICATION NUMBER: PCT/SE96/01558
/ EARLIER FILING DATE: 1996-11-28
/ EARLIER APPLICATION NUMBER: SE 9504272-7
/ EARLIER FILING DATE: 1995-11-29
/ EARLIER APPLICATION NUMBER: SE 9601506-0
/ EARLIER FILING DATE: 1996-04-19
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 3074
/ TYPE: DNA
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: Description of Unknown Organism:beli gene
/ OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
/ OTHER INFORMATION: (potato)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (189)..(2825)
/ FEATURE:
/ NAME/KEY: sig_peptide
/ LOCATION: (189)..(332)
/ FEATURE:
/ NAME/KEY: mat_peptide
/ LOCATION: (333)..(2825)
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (92)..(2156)
/ OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are
/ OTHER INFORMATION: n wherein n = A, C, G or T.
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (285)..(287)
/ OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu, Val
/ OTHER INFORMATION: or Phe.
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1407)..(1406)
/ OTHER INFORMATION: Amino acid 358 is Xaa wherein Xaa = Leu or Phe.
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1428)..(1430)
/ OTHER INFORMATION: Amino acid 366 is Xaa wherein Xaa = Thr.
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1896)..(1898)
/ OTHER INFORMATION: Amino acid 522 is Xaa wherein Xaa = Tyr, Ser, Cys
/ OTHER INFORMATION: or Phe.
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (2154)..(2156)
/ OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro.
/ US-09-087-277-1
/
/ Query Match 4.6%; Score 94; DB 3; Length 3074;
/ Best Local Similarity 78.9%; Pred. No. 4,2e-15;
/ Matches 112; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
/
/ QY 1909 TTCTAGATGACATTACTGCGAAGTATGCGAATATTTGGATTGCTACTGATGTTGAT 1968
/ DB 1740 TTATCGGTGGATTCTCTGGAACTACGAGAACTACTTGATCGGAAGTGAATGAT 1799
/
/ QY 1969 GCGGTAGTTACTTGATGCTGTCACGATCTAATTCAGGACTTATTCGTGATGCTGA 2028
/ DB 1800 GCTGTGTATCTGATGCTGTCACGATCTTATTCATGGGCTTTCCAGATGCAATT 1859
/
/ QY 2029 TCCATTGTTGAAGATGTAAGTG 2050
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MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/330,330  
FILING DATE: 11-JUN-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 10-181455  
FILING DATE: 12-JUN-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Ph.D., J.D., Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 06501/032001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10322 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
US-09-330-330-3

Query Match 3.6%; Score 74.4; DB 3; Length 10322;  
Best Local Similarity 63.6%; Pred. No. 1.2e-09;  
Matches 145; Conservative 0; Mismatches 81; Indels 2; Gaps 2;

QY 961 TTGTGCTTAAGTCAAACTTTTAAAGTTGACCAAGCTTATGGAATAATATCAATC 1020  
DB 4998 TTTTTCAGTCAAACTTTTAAAGTTGACCAAGCTTATGGAATAATATCAATC 5056  
QY 1021 TACAACCAAAATCTTATGATCAGAT-TAACAAATTTTATTTATATAGCAATC 1079  
DB 5057 TCCACACGAATTTGTTTCAATTAATGATGCAATTAATATTTGATGATGTTTGT 5116  
QY 1080 TTGTATGTTGATATATGACACATTTTCTATAGACTGTTCAAAATATAGAGAAGTTG 1139  
DB 5117 TTTGTTGAATATGCTGCTATATTTTAAAAAAGTTGCTCAACCTTAACAGATTG 5176  
QY 1140 ACTTGGACAAATCTAGAACTTCAATCAATTTGGATGACAGGAAACAT 1187  
DB 5177 ACTAGAGAAAGTCAAGACGCTTATATATGAAATAGAGGAGAAAT 5224

## RESULT 14

US-09-257-894-25  
Sequence 25, Application US/09257894  
Patent No. 6376749

GENERAL INFORMATION:  
APPLICANT: Broglie, Karen E.  
APPLICANT: Klein, Theodore M.  
APPLICANT: Hubbard, Natalie L.  
APPLICANT: Lightner, Jonathan E.  
TITLE OF INVENTION: No. 6376749el Starches via Modification of  
TITLE OF INVENTION: Expression of Starch Biosynthesis  
NUMBER OF SEQUENCES: 25

## CORRESPONDENCE ADDRESS:

ADDRESSEE: E. I. du Pont de Nemours and Company  
STREET: 1007 Market Street  
CITY: Wilmington  
STATE: Delaware  
COUNTRY: USA  
ZIP: 19898

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Microsoft Windows 95  
SOFTWARE: Version 7.0A  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/257,894  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/091,052  
FILING DATE: JUNE 10, 1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Majarian, William R.  
REGISTRATION NUMBER: 41,173  
REFERENCE/DOCKET NUMBER: BB-1066-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 302-992-4926  
TELEFAX: 302-773-0164  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1809 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-257-894-25

Query Match 3.5%; Score 71.2; DB 4; Length 1809;  
Best Local Similarity 69.3%; Pred. No. 3.7e-09;  
Matches 97; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 271 TTGTGCTTGGCTTTCAGAGTACCATGTTACTAATTTTTCACCAAGTGCCTTTT 330  
DB 895 TCGACTATGCTTCTTTCGAGTACCATGACAAATTTCTTTCGCTTAGCAGCATCA 954  
QY 331 GGAATCCAGAGAGCTTAAATCCTTGATGATGATGAGACATGAGCTGGTTGCTGTT 390  
DB 955 GGCACACAGAGAGCTTCAATATCTTGTGATTAAGGACACAGTTGGGTTTGGAGTT 1014  
QY 391 CTATGATATTTGTTCAATAG 410  
DB 1015 CTGATGATGTTGTCATAG 1034

## RESULT 15

US-09-257-894-20  
Sequence 20, Application US/09257894  
Patent No. 6376749

GENERAL INFORMATION:  
APPLICANT: Broglie, Karen E.  
APPLICANT: Klein, Theodore M.  
APPLICANT: Hubbard, Natalie L.  
APPLICANT: Lightner, Jonathan E.  
TITLE OF INVENTION: No. 6376749el Starches via Modification of  
TITLE OF INVENTION: Expression of Starch Biosynthesis  
NUMBER OF SEQUENCES: 25

## CORRESPONDENCE ADDRESS:

ADDRESSEE: E. I. du Pont de Nemours and Company  
STREET: 1007 Market Street  
CITY: Wilmington  
STATE: Delaware  
COUNTRY: USA  
ZIP: 19898

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Microsoft Windows 95  
SOFTWARE: Version 7.0A  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/257,894  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/091,052  
FILING DATE: JUNE 10, 1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Majarian, William R.

Mon Apr 12 10:24:24 2004

us-09-508-377-10\_copy\_4818\_6867.rn1

Page 8

/ REGISTRATION NUMBER: 41,173  
/ REFERENCE/DOCKET NUMBER: BB-1066-A  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 302-392-4926  
/ TELEFAX: 302-773-0164  
/ INFORMATION FOR SEQ ID NO: 20:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 1865 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: cDNA  
US-09-257-894-20

Query Match 3.5%; Score 71.2; DB 4; Length 1865;  
Best Local Similarity 69.3%; Pred. No. 3.8e-09;  
Matches 97; Conservative 0; Mismatches 43; Indels 0; Gaps 0;  
QY 271 TTGTTGTTGCGCTTGTTCAGGTACCATGTACTAATTTTTCACCAAGTAGCCGTTT 330  
DB 951 TCGTACTATGCTTCTTTCGGGTACCATGTGCAATTTCTTTCGGTTAGCAGCATCA 1010  
QY 331 GGAAGTCGAGAGAGCTTAAATCCTTGATCGATAGAGCAGATGAGCTTGGTTGCTGTT 390  
DB 1011 GGCACACGAGAGAGCTCAATATCTGTGTATAGGACACAGTTGGGTTTGGAGATT 1070  
QY 391 CTTATGATATGTTGTCATAG 410  
DB 1071 CTGATGATGTGTGCCATAG 1090

Search completed: April 10, 2004, 14:13:12  
Job time : 150.768 secs



QY 121 TATTACACAAATGCAATTTTCTGTATACAC-TCTTACCCCATTTGAGCTTATACATC 179  
DB 4940 TATTACACAAATGCAATTTTCTGTATACAC-TCTTACCCCATTTGAGCTTATACATC 4999  
QY 180 CTATGCTTATGACATTAATAATTTGGATATATCCTTTATATAGATATAGTACAAAC 239  
DB 5000 CTATGCTTATGACATTAATAATTTGGATATATCCTTTATATAGATATAGTACAAAC 5059  
QY 240 TACACTTAGATTTG--AAAAAGATCTTTATTTGTTGGCTTGTCCAGGTACCA 296  
DB 5060 TACACTTAGATTTGANNANANAGATCTTTATTTGTTGGCTTGTCCAGGTACCA 5119  
QY 297 TGTACTAATTTTTTGGACCAAGTACCCCTTTGGATCTCCAGAGCACTTAAATCCCTT 356  
DB 5120 TGTACTAATTTTTTGGACCAAGTACCCCTTTGGATCTCCAGAGCACTTAAATCCCTT 5179  
QY 357 GATGATAGACACATGAGCTTGGTTGGCTTGTCTTATGATATTTGTCATAGGTAAT 416  
DB 5180 GATGATAGACACATGAGCTTGGTTGGCTTGTCTTATGATATTTGTCATAGGTAAT 5239  
QY 417 AGTCCAAATTTAATTTAGCTGTTTACTGTTTATCTGTTATCTTAAAGGAAATTCAGGC 476  
DB 5240 AGTCCAAATTTAATTTAGCTGTTTACTGTTTATCTGTTATCTTAAAGGAAATTCAGGC 5299  
QY 477 AATTATATATCATTTGTCAAAGCTTAAGATGGCGAAAGTGAATGTCAAAATCTAGAGTG 536  
DB 5300 AATTATATATCATTTGTCAAAGCTTAAGATGGCGAAAGTGAATGTCAAAATCTAGAGTG 5359  
QY 537 GCATTAAGAAAAATGGCAAAAAGTGAAGTGGCAAAAATTTTCCATCCCTAAATGG 596  
DB 5360 GCATTAAGAAAAATGGCAAAAAGTGAAGTGGCGAAAAAATTTTCCATCCCTAAATGG 5419  
QY 597 CAGGAGCCCTATCGCGCAATATTTTCCATCTATTAATTTGCTAGCTGACTCTTTT 656  
DB 5420 CAGGAGCCCTATCGCGCAATATTTTCCATCTATTAATTTGCTAGCTGACTCTTTT 5479  
QY 657 TCTCAGATGATTAACCAAGTTGACATGGAATGATTTGGTACCTGTATAGTAACTGACA 716  
DB 5480 TCTCAGATGATTAACCAAGTTGACATGGAATGATTTGGTACCTGTATAGTAACTGACA 5539  
QY 717 GTTCCATAGAAATATCGTTTGAATGGCAACAATTTGATGCCATAGTGGACTATGAG 776  
DB 5540 GTTCCATAGAAATATCGTTTGAATGGCAACAATTTGATGCCATAGTGGACTATGAG 5599  
QY 777 AAGTTAGAGTCTATCATATAGAAATTAATCAACTGGCCATGTACTGTGGCACTACATATA 836  
DB 5600 AAGTTAGAGTCTATCATATAGAAATTAATCAACTGGCCATGTACTGTGGCACTACATATA 5659  
QY 837 GTTGGCAAGTTGAAAACTGACAGCAATACCTCACTGATAGTGGCCAGGCCCACTTGC 896  
DB 5660 GTTGGCAAGTTGAAAACTGACAGCAATACCTCACTGATAGTGGCCAGGCCCACTTGC 5719  
QY 897 CAGCTTATATAGATGTTACTCCCTGTGAATCATTTGAACTATTAATTAAGTTTC 956  
DB 5720 CAGCTTATATAGATGTTACTCCCTGTGAATCATTTGAACTATTAATTAAGTTTC 5779  
QY 957 TTCATTTGTCTAAGTCAAACTTCTTAAGTTTGACCAAGTCTATGAAAAATATATCAA 1016  
DB 5780 TTCATTTGTCTAAGTCAAACTTCTTAAGTTTGACCAAGTCTATGAAAAATATATCAA 5839  
QY 1017 CATCTAACAACCAATTAATCTTGTATCAGATTAACAATTTTATTTTATATATAGCAC 1076  
DB 5840 CATCTAACAACCAATTAATCTTGTATCAGATTAACAATTTTATTTATATATATAGCAC 5899  
QY 1077 ATCTTTGATGTTGATATATAGACATATTTTCTATAGACTTGTCAAAATATAGAGAGT 1136  
DB 5900 ATCTTTGATGTTGATATATAGACATATTTTCTATAGACTTGTGTCAAAATATAGAGAGT 5959  
QY 1137 TTGACTTATGACAAATCTTGAATCTTGAATTTGATGAGAGGAACTCAAAATATA 1196  
DB 5960 TTGACTTATGACAAATCTTGAATCTTGAATTTGATGAGAGGAACTCAAAATATA 6019

QY 1197 TAGATAGATGCAACACTTCAACAAAAAATGACACCTTGTCAACATATATGATCAGAC 1256  
DB 6020 TAGATAGATGCAACACTTCAACAAAAAATGACACCTTGTCAACATATATGATCAGAC 6079  
QY 1257 CATCTGTTGCTTTAGCCACTTGTCTTCAATTTATATGTTTGTAGCTTAATCTACTTTC 1316  
DB 6080 CATCTGTTGCTTTAGCCACTTGTCTTCAATTTATATGTTTGTAGCTTAATCTACTTTC 6139  
QY 1317 CTCTTACTGTTGTTGTTGATTTATTTTCAAGTTGCAATGCTTCTATCAATATTTTGTGA 1376  
DB 6140 CTCTTACTGTTGTTGTTGATTTATTTTCAAGTTGCAATGCTTCTATCAATATTTTGTGA 6199  
QY 1377 CCTGTGACATTCGCAAAATTAATACCTTGAAGGTTGATGATGCTTGAATGACATGAT 1436  
DB 6200 CCTGTGACATTCGCAAAATTAATACCTTGAAGGTTGATGATGCTTGAATGACATGAT 6259  
QY 1437 ACAATTAATCTTCCAGGTTCCAGCGGCAATCATTTGATGAGATTTCTGTATTC 1496  
DB 6260 ACAATTAATCTTCCAGGTTCCAGCGGCAATCATTTGATGAGATTTCTGTATTC 6319  
QY 1497 AACTATGGAATTTGGAAATGATGCTGATCTGATCTCTGTACCAATTTGGCTTACTGT 1556  
DB 6320 AACTATGGAATTTGGAAATGATGCTGATCTGATCTCTGTACCAATTTGGCTTACTGT 6379  
QY 1557 CCTGTATCTGTCTTACACATGTTGATATCTTATCTTATGACAGTATTTGATTTCTT 1616  
DB 6380 CCTGTATCTGTCTTACACATGTTGATATCTTATCTTATGACAGTATTTGATTTCTT 6439  
QY 1617 ACTGTCAAACCGAGATGTTGCTTGAAGAATTAAGTTGATGATTTGATTTGATG 1676  
DB 6440 ACTGTCAAACCGAGATGTTGCTTGAAGAATTAAGTTGATGATTTGATTTGATG 6499  
QY 1677 GGTGACCTCCATGATGATATACCATGATTAACAAGTATGATCAAGGTTTACTAGT 1736  
DB 6500 GGTGACCTCCATGATGATATACCATGATTAACAAGTATGATCAAGGTTTACTAGT 6559  
QY 1737 AACTTTTATGAGGCACTGAAACAATGCTATGATCATTAACATGATCATGATCAGAGCT 1796  
DB 6560 AACTTTTATGAGGCACTGAAACAATGCTATGATCATTAACATGATCATGATCAGAGCT 6619  
QY 1797 TGTGTACGAGTCTTAGATGATTCCTTAGATGCTTGTGAACAATTTTACTGATGATC 1856  
DB 6620 TGTGTACGAGTCTTAGATGATTCCTTAGATGCTTGTGTGAACAATTTTACTGATGATC 6679  
QY 1857 ATGGAAGATTTGGAAGGATTAATTTTCTTCTAGATTTGCTTCTGATCTAGAT 1916  
DB 6680 ATGGAAGATTTGGAAGGATTAATTTTCTTCTAGATTTGCTTCTGATCTAGAT 6739  
QY 1917 GACATTTACTGGAACATATGCGCAATATTTTGGATTTGCTATGATGATGCGGTAGT 1976  
DB 6740 GACATTTACTGGAACATATGCGCAATATTTTGGATTTGCTATGATGATGCGGTAGT 6799  
QY 1977 TTAATGATGCTGTGCAACGATTAATTCATGACCTTATCTGATGCTGTATCCATTTGG 2036  
DB 6800 TTAATGATGCTGTGCAACGATTAATTCATGACCTTATCTGATGCTGTATCCATTTGG 6859  
QY 2037 TGAAGATGTAAGTG 2050  
DB 6860 TGAAGATGTAAGTG 6873

RESULT 2  
US-10-434-893A-1  
Sequence 1, Application US/10434893A  
Publication No. US2004006083A1  
GENERAL INFORMATION:  
APPLICANT: Ahmed Regina  
APPLICANT: Matthew Kennedy Morell  
APPLICANT: Sadequr Rahman  
TITLE OF INVENTION: Barley with altered branching enzyme activity and starch and suc  
TITLE OF INVENTION: containing products with an increased amylose content  
FILE REFERENCE: 69425  
CURRENT APPLICATION NUMBER: US/10/434, 893A

ପାଞ୍ଚେ ୩

Accession	Sequence	Position
Db	ATCTAATATTATTGATGTCCTCCCTGATCCAAATTTGATTGAAGTCTAGATTGTGCTTAA	5965
Db	6024	
Qy	GTCAAACTCTTTAGTTTGACCAAGCTCTTGGAAAAATATATCAATCATGACAAACCA	1030
Qy	971	
Db	5964	
Db	GTCAAACTTCTCTAATTGACCAAGCTCTAATAGAAAATGTGCTGATATCTACAAATCA	5905
Qy	1031	
Qy	AATTACTTGATGATGATTAACAATTTTATTATTATTAATTATGACACATCTTTGATGTG	1090
Db	5904	
Db	AAATGTGCTAATATATAAATAAATAAATTTGTTAATCTGATCAAAAGTAATTTGGTGTGT	5845

5844 AGATGTTGATATATTTTCCAAATAGACTTGTGTAACCTTAAGAGTTTGACTTAGACAA 57855

Db 5784 ATGAAGACTTTAAGTATATGTTCAATGATCAACAGGAGTACAT 5734

RESULT 4  
US-10-260-238-1027  
Sequence 1027, Application US/10260238

```

1  GENERAL INFORMATION:
2  APPLICANT: Budworth, Paul R.
3  APPLICANT: Moughamer, Todd G.

```

APPLICANT: Briggs, Brevett E.  
APPLICANT: Cooper, Irel  
APPLICANT: Glazebrook, Jane  
APPLICANT: Golf, Stephen A.  
APPLICANT:

APPLICANT: katagiri, fumiaki  
APPLICANT: kreps, joel  
APPLICANT: provart, nicholas  
APPLICANT: ricke, darrell

APPLICANT: Zhu, Tong  
TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION  
FILE REFERENCE: 6011.1-NP  
CURRENT APPLICATION NUMBER: US/10/260.238

; PRIOR FILING DATE: 2001-09-26  
 ; PRIOR APPLICATION NUMBER: US 60/325,277  
 ; PRIOR FILING DATE: 2001-09-26  
 ; PRIOR APPLICATION NUMBER: US 60/370,620

```

; SEQ ID NO 1027
;
; LENGTH: 1642
;
; TYPE: DNA
;
; ORGANISM: Oryza sativa
US-10-260-238-1027

Query Match          Score 112.4; DB 15; Length 1642;
Best Local Similarity 83.18;
Matches 128; Conservative 0; Pred. No. 1,3e-15; Indels 0; Gaps 0;
Mismatch 26;

```

1373 TGTAACCTGCAGTCATTCGTCAATAATACCCTTGACGGTTTGAATGGTTTCATGGCAC 1432

Db 323 TGTTACAGCAGCCATGCGTCAATAATACCCTAGATGGGTGAACGGTTTGTGATGGTAC 382

QY 1433 TGATACACATTACTTCACCGGTGTGCACGGCCCATCTTGATGTGGGATTCTCGCTT 14922

D5 383 AGATACGCATTACTTCATAGTGTGTTCAACGGGCCCATCATTTGGAGTGGGATTCTGGCCT 442

Qy 1493 ATTCACTATGGGAGTTGGGAGTATGACTCT 1526

D6 443 TTTCACATATGGGAATTGGGAAGTCTCAGAATT 476

## RESULT 5

US-10-434-893A-4  
; Sequence 4, Application US/10434893A

5784 ATGAAGACTTAAAGTAAATATGTTCAATGAATTCACAGGAGTAACAT 5734

RESULT 4  
US-10-260-238-1027

Sequence 1027, Application US/10260238  
Publication No. US20040016025A1  
GENERAL INFORMATION:  
APPLICANT: Budworth, Paul R.

APPLICANT: Moughamer, Todd G.  
APPLICANT: Briggs, Steven P.  
APPLICANT: Cooper, Bret  
APPLICANT: Glazebrook, Jane

APPLICANT: Goff, Stephen A.  
APPLICANT: Katagiri, Fumiyaki  
APPLICANT: Kreps, Joel  
APPLICANT: Prost, Nicholas

APPLICANT: Ricke, Darrell  
 APPLICANT: Zhu, Tong  
 TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION  
 INVENTOR: 0011, ND

1 CURRENT APPLICATION NUMBER: US/10/260,238  
 2  
 3 CURRENT FILING DATE: 2002-09-26  
 4  
 5 PRIOR APPLICATION NUMBER: US 60/325,448

7 PRIOR APPLICATION NUMBER: US 60/325,277  
 7 PRIOR FILING DATE: 2001-09-26  
 7 PRIOR APPLICATION NUMBER: US 60/370,620

? PRIOR FILING DATE: 2002-04-04  
 ? NUMBER OF SEQ ID NOS: 6077  
 ? SEQ ID NO 1027  
 ? LENGTH: 1642

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!      TYPE: DNA
!      ORGANISM: Oryza sativa
US-10-260-238-1027

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Query Match	5.5%;	Score 112.4;	DB 15;	length 1642;
Best Local Similarity	83.1%;	Pred. 1.3e-15;		
Matches 128;	Conservative	0;	Mismatches 26;	Indels 0;
			Gaps	0;

Qy 1373 TGTATACCTGCAAGTCATTCGTCAATATATACCTTGAACGGTTTAAATGGTTTCGATGGCAC 1432

Db 323 TGTTCACAGCAACCCATCGCTCAATATATACCTAGATGGGTGAACGGTTTATATGGTAC 382

QY	1433	AGATACACATTACTTCCACCGGCGTCCACGCGGCATTCATTGGATGTGGATCTCGCTT	1492
Db	383	AGATACCCATTACTTTCATAGTGGTTACGCGGCCATTCATTGGATGTGGATCTTCGCTT	442

QY	1493	ATTCACTATGGAGTGGGAGTATGTAGCTCT	1526
Db	443	TTTCAACTATGGAGATTGGGAGTCTTAGAGATT	476

100

US-10-434-893A-4

Publication No. US2004006083A1

```

? GENERAL INFORMATION:
? APPLICANT: Ahmed Regina
? APPLICANT: Matthew Kennedy Morell
? APPLICANT: Sadequr Rahman
? TITLE OF INVENTION: Barley with altered branching enzyme activity and starch and starch
? TITLE OF INVENTION: containing products with an increased amylose content
? FILE REFERENCE: 69425
? CURRENT APPLICATION NUMBER: US/10//434,893A
? CURRENT FILING DATE: 2003-05-09
? NUMBER OF SEQ ID NOS: 11
? SOFTWARE: PatentIn version 2.1
? SEQ ID NO 4
? LENGTH: 6550
? TYPE: DNA
? ORGANISM: Aegilops tauschii
? FEATURE:
? NAME/KEY: MISC_FEATURE
? LOCATION: (1)...(6550)
? OTHER INFORMATION: n is a, c, g or t
? FEATURE:
? OTHER INFORMATION: partial SSBE11b gene
? US-10-454-893A-4

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Query Match	5.5%	Score 112.2;	DB 12;	Length 6550;
Best Local Similarity	74.6%;	Pred. No. 3.1e-15;		
Matches 141;	Conservative	0;	Mismatches 48;	Indels 0;
				Gaps 0;

QY	256	AAAAGATCAATTATATGTTGTGGCTGTGTCAGAGTCCAGTACCAATTTTATTCGA	315
Db	4984	AATACCACTTTTATAGTGTGTTTACTCTTATTCAGATCCATGTTACCAATTTCTTTGCA	5044
QY	316	CCAGTAGCCGCTTTTGGACTCCAGAGCACTAAATCTTGATCGATAGACATGAG	375
Db	5044	CCAGTAGCCGCTTTTGGGCTCCCAAGAGATTAAATCTTGATGATAGAGCTCACAG	5102
QY	376	CTTGCTTGCCTGTGTTCTTATGAGATATGTTCAATAGTAATTAATTCACATTTTAA	435
Db	5104	CTTGCTTGTGTTGTCTCATGAGATGTTGTTACACAGTACTTAATGAAATTTGAGGTTG	5163
QY	436	TGTTTACT	444
Db	5164	GTGTTAAGT	5172

RESULT 6  
US-10-260-238-2253  
; Sequence 2253, Application US/10260238  
; Publication No. US20040016025A1  
; GENERAL INFORMATION:

APPLICANT: Budworth, Paul R.  
 APPLICANT: Moughamer, Todd G.  
 APPLICANT: Briggs, Steven P.  
 APPLICANT: Cooper, Bret  
 APPLICANT: Glazebrook, Jane  
 APPLICANT: Goff, Stephen A.  
 APPLICANT: Katagiri, Fumiyuki  
 APPLICANT: Kleps, Joel  
 APPLICANT: Provart, Nicholas  
 APPLICANT: Ricke, Darrell  
 APPLICANT: Zhu, Tong  
 TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION  
 FILE REFERENCE: 60111-NP  
 CURRENT APPLICATION NUMBER: US/10/260,238  
 CURRENT FILING DATE: 2002-09-26  
 PRIOR APPLICATION NUMBER: US 60/325,448  
 PRIOR FILING DATE: 2001-09-26  
 PRIOR APPLICATION NUMBER: US 60/325,277  
 PRIOR FILING DATE: 2001-09-26  
 PRIOR APPLICATION NUMBER: US 60/370,620  
 PRIOR FILING DATE: 2002-04-04  
 NUMBER OF SEQ ID NOS: 6077  
 SEQ ID NO 2253

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; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-260-238-2253

```

Query Match	5.4%	Score 110.6	DB 15	Length 2000
Best Local Similarity	66.9%	Pred. No. 3	9e-15	
Matches 172, Conservative	0	Mismatches 84	Indels 1	Gaps 1

Qy	940	CAATTCTCTTAAAGTTCCTGATTCCTGCTAAGTCAAACTTCTTAAAGTTGACCAAGCT	999
Db	817	CAATTCTCTTAAAGTTCCTGATTCCTGCTAAGTCAAACTTCTTAAAGTTGACCAAGCT	876
Qy	1000	ATTGGAATAATATCAACATCTACACACCAAAATTAAGTTGATCAGATTAAACAAATTTTAA	1055
Db	877	ATTGGAATAATATCAACATCTACACACCAAAATTAAGTTGATCAGATTAAACAAATTTTAA	936
Qy	1060	TTTATATATATATGACATCTTGATCTGTGTGAGTATACAGACACTTTTCTATAGACTGT	1119
Db	937	TATTTATATATATGATCTTGATCTGTGTGAGTATATGATCAATATTTTCTACAACTGT	996
Qy	1120	GTCAAA-TATAGAGAGTTGACTTTAGACAAATCTAGAACTTCAATCAATTTGGATCAG	1178
Db	997	GTCAAACTTTAAAAAGTTTGACAAAGAAAAAGTCAAGGAGCTTATATATAGAAATGG	1056
Qy	1179	AGGAGACATCAAAATAT 1195	
Db	1057	AAGGAGTATTTAATACT 1073	

RESULT 7  
US-10-397-954A-1

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1      Sequence 1, Application US/10397954A
2      Publication No. US20030221220A1
3
4      GENERAL INFORMATION:
5
6      APPLICANT: Pearlstein, Richard W.
7      APPLICANT: Broglie, Karen E.
8      APPLICANT: Hines, Christopher F.
9      TITLE OR INVENTION: Maize Starch Containing Elevated Amounts of Actual Amylose
10
11      FILE REFERENCE: BB1510 US NA
12
13      CURRENT APPLICATION NUMBER: US/10/397,954A
14
15      CURRENT FILING DATE: 2003-03-26
16
17      PRIOR APPLICATION NUMBER: 60/368,387
18
19      PRIOR FILING DATE: 2002-03-27
20
21      PRIOR APPLICATION NUMBER: 60/381,534
22
23      PRIOR FILING DATE: 2002-05-16
24
25      NUMBER OF SEQ ID NOS: 6
26
27      SOFTWARE: Microsoft Word 97
28
29      SEQ ID NO: 1
30
31      LENGTH: 2443
32
33      TYPE: DNA
34
35      ORGANISM: Artificial Sequence
36
37      FEATURE:
38
39      NAME/KEY: misc feature
40      LOCATION: (1)_(2443)
41
42      OTHER INFORMATION: SEQID modified region
43
44      US-10-397-954A-1

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Query Match	5.1%	Score	105.2	DB	15	Length	2443
Best Local Similarity	83.8%	Pred. No.	7.8e-14				
Matches	119	Conservative	0	Mismatches	23	Indels	0
						Gaps	0

QY	1909	TTCTAGATGACATTTACTGGGAACTATGGCCAAATTTTGGATTGGCTACTGAGTGTAT	1966
Db	1029	TTACAAGTAACATTTACGGGAACTCTCATTAGATATTTGGCTTGGCCACCGATGTAAAT	1088
QY	1969	GCGGTAGTTTACTGATGCTGGTCAAGATCTAATTCATGGACTTATCCGTAGTCTGA	2022
Db	1089	GCACTGGTTTACTTGATGCTGGTAAATGATCTAATTCATGGACTTATCCGTAGGCTGTA	1148
QY	2029	TCGATTGGTGAAGATGTAAGTG	2050
Db	1149	ACCATGGTGAAGATGTTAGTG	1170

RESULT 8  
US-09-792-127-1

/ Sequence 1, Application US/09792127  
/ Patent No. US2002002713A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Allen, Steve  
/ APPLICANT: Beckles, Diane M.  
/ APPLICANT: Butler, Karla  
/ APPLICANT: Pearlstein, Rich  
/ TITLE OF INVENTION: Starch Branching Enzyme IIb  
/ FILE REFERENCE: B01439 US NA  
/ CURRENT APPLICATION NUMBER: US/09/792,127  
/ PRIOR FILING DATE: 2001-02-23  
/ PRIOR APPLICATION NUMBER: 60/186098  
/ NUMBER OF SEQ ID NOS: 5  
/ SOFTWARE: Microsoft Office 97  
/ SEQ ID NO: 1  
/ LENGTH: 2559  
/ TYPE: DNA  
/ ORGANISM: Triticum aestivum  
US-09-792-127-1

Query Match 5.1%; Score 105; DB 9; Length 2559;  
Best Local Similarity 82.8%; Pred. No. 8.8e-14;

Matches 120; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

DB 1382 CAGTCAATTCGTAATATATACCTTGACGGTTGAAATGGTTTCGATGGCACTGATACACA 1441

QY 827 CAGTCAACGGTCAATATATACCTTGACGGTTGAAATGGTTTCGATGGCACTGATACACA 886

DB 1442 TTACTTCCACGGTGTCCACGGCCCATCATGATGGATGTTCTGTTTCACTA 1501

QY 887 TTACTTCCACGGTGTCCACGGCCCATCATGATGGATGTTCTGTTTCACTA 946

DB 1502 TGGGAGTTGGGAGATATATAGCTCT 1526

QY 947 TGGGAGTAAAGAGATATATAGGTTT 971

## RESULT 9

US-09-792-127-3  
/ Sequence 3, Application US/09792127  
/ Patent No. US2002002713A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Allen, Steve  
/ APPLICANT: Beckles, Diane M.  
/ APPLICANT: Butler, Karla  
/ APPLICANT: Pearlstein, Rich  
/ TITLE OF INVENTION: Starch Branching Enzyme IIb  
/ FILE REFERENCE: B01439 US NA  
/ CURRENT APPLICATION NUMBER: US/09/792,127  
/ PRIOR FILING DATE: 2001-02-23  
/ PRIOR APPLICATION NUMBER: 60/186098  
/ NUMBER OF SEQ ID NOS: 5  
/ SOFTWARE: Microsoft Office 97  
/ SEQ ID NO: 3  
/ LENGTH: 3039  
/ TYPE: DNA  
/ ORGANISM: Triticum aestivum  
US-09-792-127-3

Query Match 5.1%; Score 105; DB 9; Length 3039;  
Best Local Similarity 82.8%; Pred. No. 9.7e-14;

Matches 120; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1382 CAGTCAATTCGTAATATATACCTTGACGGTTGAAATGGTTTCGATGGCACTGATACACA 1441

DB 1307 CAGTCAACGGTCAATATATACCTTGACGGTTGAAATGGTTTCGATGGCACTGATACACA 1366

DB 1367 TTACTTCATGGCGGTTACGGGCGCATCATGATGGGATTCGCCGTGTTTACTA 1426

QY 1502 TGGGAGTTGGGAGATATATAGCTCT 1526

DB 1427 TGGGAGTAAAGAGATATATAGGTTT 1451

RESULT 10  
US-10-434-893A-2

/ Sequence 2, Application US/10434893A  
/ Publication No. US20040060083A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Ahmed Regina  
/ APPLICANT: Matthew Kennedy Morell  
/ APPLICANT: Sadequr Rahman  
/ TITLE OF INVENTION: Barley with altered starch branching enzyme activity and starch and sta  
/ FILE REFERENCE: 69425  
/ CURRENT APPLICATION NUMBER: US/10/434,893A  
/ PRIOR FILING DATE: 2003-05-09  
/ NUMBER OF SEQ ID NOS: 11  
/ SOFTWARE: PatentIn version 2.1  
/ SEQ ID NO: 2  
/ LENGTH: 2780  
/ TYPE: DNA  
/ ORGANISM: Hordeum vulgare  
/ FEATURE:  
/ OTHER INFORMATION: SSBElIb cDNA  
US-10-434-893A-2

Query Match 5.0%; Score 101.8; DB 12; Length 2780;  
Best Local Similarity 77.0%; Pred. No. 5.1e-13;

Matches 124; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 290 GGTACCATGTTACTAATTTTGTGACCAAGTACCGTTTGAATCCGAGAGACTTAA 349

DB 1115 GGTACCATGTTACTAATTTTGTGACCAAGTACCGTTTGAATCCGAGAGACTTAA 1174

QY 350 AATCCTTGATGATAGACACATGAGCTTGTCTGTTCTTATGATATTTGTTCA 409

DB 1175 AATCCTTGATGATAGACACATGAGCTTGTCTGTTCTTATGATATTTGTTCA 1234

QY 410 GGTAAATAGTCCAAATTTTATTTAGCTGTTTACTGTTAT 450

DB 1235 GTCAAGCATCAAGTAAATACCTTGACGGTTGAAATGTTT 1275

## RESULT 11

US-10-260-238-2253/C  
/ Sequence 2253, Application US/10260238  
/ Publication No. US20040016025A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Budworth, Paul R.  
/ APPLICANT: Moughamer, Todd G.  
/ APPLICANT: Briggs, Steven P.  
/ APPLICANT: Cooper, Bret  
/ APPLICANT: Glazebrook, Jane  
/ APPLICANT: Goff, Stephen A.  
/ APPLICANT: Katagiri, Fumiyaki  
/ APPLICANT: Krieds, Joel  
/ APPLICANT: Provart, Nicholas  
/ APPLICANT: Riche, Darrell  
/ APPLICANT: Zhu, Tong  
/ TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION  
/ FILE REFERENCE: 60111-NP  
/ CURRENT APPLICATION NUMBER: US/10/260,238  
/ PRIOR FILING DATE: 2002-09-26  
/ PRIOR APPLICATION NUMBER: US 60/325,448  
/ PRIOR FILING DATE: 2001-09-26  
/ PRIOR APPLICATION NUMBER: US 60/325,277  
/ PRIOR FILING DATE: 2001-09-26

Query Match 5.1%; Score 105; DB 9; Length 3039;  
Best Local Similarity 82.8%; Pred. No. 9.7e-14;

Matches 120; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1382 CAGTCAATTCGTAATATATACCTTGACGGTTGAAATGGTTTCGATGGCACTGATACACA 1441

DB 1307 CAGTCAACGGTCAATATATACCTTGACGGTTGAAATGGTTTCGATGGCACTGATACACA 1366





Mon Apr 12 10:24:24 2004

us-09-508-377-10\_copy\_4818\_6867.rnpb

Page 7

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Matches 112; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
QY 1909 TTCTAGATGACATTTACTGGGACATGCGAATATTTTGGATTTGCTACTGATGTGAT 1968
Db 734 TTATCGGCGGATTCACCTGAGAACTACAGAGAACTTTGGCTGCGAATGATGTGAT 793
QY 1969 GCGGTAGTTTACTGATGCTGCTGCAACGATCTAATTCATGAGCTTTATCCTGATGCTGA 2028
Db 794 GCTGTGTGATCTGATCTGCTGCTGCAACGATCTTATTCATGAGGCTTTCCAGATGCAAT 853
QY 2029 TCCATTGCTGAAGATGTAAGTG 2050
Db 854 ACCATTGGTGAAGATGTTAGCG 875

RESULT 14
US-10-260-238-2424
; Sequence 2424, Application US/10260238
; Publication No. US20040016025A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.
; APPLICANT: Moughamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Karagiri, Fumiyaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicholas
; APPLICANT: Rieke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
; FILE REFERENCE: 60111-NP
; CURRENT APPLICATION NUMBER: US/10/260,238
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/325,448
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 6077
; SEQ ID NO 2424
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Oryza sativa
; US-10-260-238-2424

Query Match 4.6%; Score 94; DB 15; Length 2000;
Best Local Similarity 62.0%; Pred. No. 2,8e-11;
Matches 165; Conservative 0; Mismatches 100; Indels 1; Gaps 1;
QY 940 CATATTTACTTAAAGTTCTTCATTTGCTCTAAGTCAAACTTTTAAAGTTTGACCAAGTCT 999
Db 512 CAGGTTATTAAGATGTTTAACTTTAGTTCGAAGTCAAACTTTTCAAGTTTGACTAAGTTT 571
QY 1000 ATTGAAAATATATGCAACATCTACACACCAAACTTTGATGATGATGATGATGATGAT 1059
Db 572 AGAGCATATATATATATATATATATATATATATATATATATATATATATATATATAT 630
QY 1060 TTTTATTTATTTAGACATCTTTGATGTTGTAGATATCAGACATTTTCTATAGACTTG 1119
Db 631 TATATTTTATATATATATTTGCTTTGGGTTGAATGTTACTATCTTTTCTTCAAACTTG 690
QY 1120 GTCAATATATAGAACTTTGACTTAGACAAATCTAGAACTTCAATCAATTTGGATCAGA 1179
Db 691 ATCAAACTTAAAGCTTTGGCTTTGATCMAAGTCAAAAGCTTTAAACCTGAAAAGGA 750
QY 1180 GGGAACTATCAATTAATATAGATAGAT 1205
Db 751 GGGAGTACATTAATTTTGAATTAAT 776
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RESULT 15
US-10-056-454A-16
; Sequence 16, Application US/10056454A
; Publication No. US20030166919A1
; GENERAL INFORMATION:
; APPLICANT: National Starch and Chemical Investment Holding Corporation
; TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: National Starch and Chemical Investment Holding Corporation
; STREET: 1000 Unidema Blvd.
; CITY: Newcastle
; STATE: Delaware
; COUNTRY: United States of America
; ZIP: 19720
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/056,454A
; FILING DATE: 25-Jun-2002
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2576 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-056-454A-16

Query Match 4.6%; Score 94; DB 14; Length 2576;
Best Local Similarity 78.9%; Pred. No. 3.2e-11;
Matches 112; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
QY 1909 TTCTAGATGACATTTACTGGGACATGCGAATATTTTGGATTTGCTACTGATGTGAT 1968
Db 1471 TTATCGGCGGATTCACCTGAGAACTACAGAGAACTTTGGCTGCGAATGATGTGAT 1530
QY 1969 GCGGTAGTTTACTGATGCTGCTGCAACGATCTAATTCATGAGCTTTATCCTGATGCTGA 2028
Db 1531 GCTGTGTGATCTGATCTGCTGCTGCAACGATCTTATTCATGAGGCTTTCCAGATGCAAT 1590
QY 2029 TCCATTGCTGAAGATGTAAGTG 2050
Db 1591 ACCATTGGTGAAGATGTTAGCG 1612
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Search completed: April 10, 2004, 20:07:35  
Job time : 729.03 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 10, 2004, 03:15:20 ; Search time 5409.32 seconds  
(without alignments)  
11317.033 Million cell updates/sec

Title: US-09-508-377-10\_COPY\_4818\_6867

Perfect score: 2050

Sequence: 1 ccgaagataatcatcatgc.....catgtggaagatgtaagt 2050

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estma:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hcc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hcc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vtc:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rdd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vtl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	250.8	12.2	930	28	CC362748 PUHLB23TD
C 2	183.8	9.0	985	29	CG882826 ZMMBB049
3	140	6.8	527	6	AL812818 Triticum
4	139.4	6.8	476	13	BU972445 HB21K16r

5	139.4	6.8	537	13	BU967331	BU967331 HB03P08r
6	134	6.5	476	13	BO245037	BO245037 TAB15032A
7	134	6.5	623	13	BU986646	BU986646 HF12102r
8	133.2	6.5	610	28	AQ576669	AQ576669 nbxb0089J
9	132.4	6.5	621	14	CD890409	CD890409 G118.114J
10	125.8	6.1	678	9	AV939010	AV939010 AV939010
11	124.4	6.1	411	13	BU970967	BU970967 HB16D15r
12	123.2	6.0	618	14	CA292638	CA292638 SCRLFL802
13	123.2	6.0	650	14	CA202517	CA202517 SCRRFL102
14	122.2	6.0	2766	11	AY109521	AY109521 Zee may8
15	121.6	5.9	399	12	BM660711	BM660711 952041B07
16	121.6	5.9	595	13	CA188662	CA188662 SCCCAM205
17	121.6	5.9	690	13	CA083722	CA083722 SCEPAM205
18	120.4	5.9	520	28	B2348549	B2348549 hp58f11.9
19	120.4	5.9	578	28	B2348550	B2348550 hp58f11.9
20	119.4	5.8	649	13	BQ840703	BQ840703 WBR4202_E
21	118.8	5.8	550	13	BU966891	BU966891 HB02K24r
22	113.8	5.6	541	29	AG213031	AG213031 Oryza sat
23	113.2	5.5	462	10	BF585594	BF585594 FM1_23_CO
24	113.2	5.5	479	28	AQ856076	AQ856076 nbxb0064F
25	113.2	5.5	821	28	AQ840558	AQ840558 nbxb0064F
26	112.6	5.5	682	14	CD938053	CD938053 OV_108019
27	110.6	5.4	852	14	CD438018	CD438018 ELO1N0508
28	110.6	5.4	871	14	CD444875	CD444875 ELO1N0445
29	110.6	5.4	2732	11	AY109532	AY109532 Zee may8
30	110.4	5.4	781	28	AQ574595	AQ574595 nbxb0085D
31	110.4	5.4	882	14	CB632953	CB632953 OST1EP11I
32	110.4	5.4	420	9	AJ465766	AJ465766 AJ465766
33	108.8	5.3	872	28	BZ667957	BZ667957 PUBG523TD
34	108.8	5.3	440	28	BZ667903	BZ667903 PUBB3M33TD
35	108.8	5.3	578	28	BZ348550	BZ348550 hp58f11.9
36	108.2	5.3	520	28	BZ348549	BZ348549 hp58f11.9
37	108.2	5.3	678	14	CA191146	CA191146 SCCCR7C0
38	108.2	5.3	821	28	AQ840558	AQ840558 nbxb0064F
39	107.4	5.2	697	29	CC992767	CC992767 ZUAEN43TV
40	107.4	5.2	736	14	CD444184	CD444184 ELO1N0436
41	106.4	5.2	548	14	CD888421	CD888421 G118.1070
42	105.6	5.2	424	14	T23385	T23385 Sc09B11 mem
43	105.4	5.1	402	12	BM660712	BM660712 952041B07
44	105.2	5.1	576	10	AW244197	AW244197 687050P06
45	105.2	5.1	636	14	CA255656	CA255656 SCEPFL418

#### ALIGNMENTS

RESULT 1  
CC362748/c  
LOCUS  
DEFINITION  
PUHLB23TD\_ZM\_0.6\_1.0\_KB\_Zee\_mays genomic clone ZMMBET475D22,  
930 bp DNA linear GSS 16-MAY-2003  
ACCSSION  
CC362748  
VERSION  
CC362748.1 GI:30832148  
KEYWORDS  
GSS.  
SOURCE  
Zee\_mays  
ORGANISM  
Zea mays  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE  
1 (bases 1 to 930)  
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,  
Resnick,A., Friess,C.M., Yuan,Y., San Miguel,P., Ma,J. and  
Bennetzen,J.  
TITLES  
JOURNAL  
Unpublished (2003)  
COMMENT  
Other GSSs: PUHLB23TB  
Contact: Cathy Whitelaw  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@tigr.org  
Seq primer: TP

FEATURES  
 Class: sheared ends.  
 Location/Qualifiers  
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 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
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 /db\_xref="taxon:4577"  
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 /note="Vector: pCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
 Cor selected genomic DNA library"

ORIGIN  
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 Best Local Similarity 65.1%; Pred. No. 3.6e-38;  
 Matches 461; Conservative 0; Mismatches 192; Indels 55; Gaps 4;  
 1343 TTGAGTTCATGCTGCTCATCATGATTTTGTGTAACCCGTCAGTCATTTGTCGAATTAATAC 1402  
 920 TTGGTTTCACTTAACCTTCTTCTTGTGTAATGCGTCAAGCTCAAGTAATAC 861  
 1403 CCTTGACGCTTGGATGTTTCGATGCGACATGATACATTAATCTTCCAGGTGTCACG 1462  
 860 TCTGGAGGGTTGATGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 801  
 1463 CGGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1522  
 800 TGGCCATCAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 743  
 1523 CTCTGATTCGTCACATATTTGGTCACTGCTCCGTATATCTGCTTCAACATGTT 1582  
 742 AACAAAAATCTCATCTCATTAATTTATTTCTCTCAATTTTCTGCTGATGCTTCA 683  
 1583 GATATTTCTATTTCTATGACGATTTGATGATTTCTTACTGTCACAGCGAGATGTTGCT 1642  
 682 ACAATTTTACCGATGATGATTTTGAATTTCTTCTCCAGTCAAGTGAATGATGATG 623  
 1643 AAGAAATTAAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1702  
 622 AGGAATTAAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 563  
 1703 ATGATTTACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1762  
 562 ACGATTAACAAGTATTAAGCTTTAGCTGTTAGTTTACT-----TCACTTGCTA 510  
 1763 GCTATGATCATATAACATGATCATGATGATGATGATGATGATGATGATGATGATGATG 1822  
 509 AGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 459  
 1823 CTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1882  
 458 ATATTTGTAATATCAATCTCTCTTCTTAATCAAAAGCA----- 419  
 1883 TATTTTCTTCTAGTTTGTCTGTTCTGATGATGATGATGATGATGATGATGATGATG 1942  
 418 -----TGATTTTACTTTAGTAACTTTTACGGGGAATCTTCAATGACT 376  
 1943 ATTTTGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2002  
 375 ATTTTGGCTTTGACACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 316  
 2003 TTCTATGATTTATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2050  
 315 TTCTATGATTTATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 268

RESULT 2  
 CG882826/c 985 bp DNA linear GSS 02-DEC-2003  
 LOCUS ZMMB0492B17f ZMMBB (HindIII) Zea mays subsp. mays genomic clone  
 DEFINITION ZMMB0492B17 5', genomic survey sequence.  
 ACCESSION CG882826  
 VERSION CG882826.1 GI:38613949

KEYWORDS  
 SOURCE GSS  
 ORGANISM Zea mays subsp. mays (maize)  
 Zea mays subsp. mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 985)  
 Bhatti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,  
 Zohovetz,V., Fuks,G., Yu,Y., Wang,R. and Messing,J.  
 Sequencing of the maize genome at FGI (2003c)  
 Unpublished (2003)  
 TITLE JOURNAL  
 COMMENT Contact: Bhatti,A.K.  
 Dr.Joachim Messing's lab  
 The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers  
 University  
 190 Frelinghuysen Road, Piscataway, NJ 08854, USA  
 Tel: 732 445 3801  
 Fax: 732 445 5735  
 Email: bhatti@waksman.rutgers.edu  
 Seq primer: 17  
 Class: BAC ends  
 High quality sequence start: 124.  
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 /lab\_host="E. coli DH10B"  
 /clone\_1db="ZMMBB (HindIII)"  
 /note="Vector: pCUG1; Site\_1: HindIII; Site\_2: HindIII"

ORIGIN  
 Query Match 9.0%; Score 183.8; DB 29; Length 985;  
 Best Local Similarity 71.0%; Pred. No. 2.6e-25;  
 Matches 306; Conservative 0; Mismatches 107; Indels 18; Gaps 4;  
 1 CGAAGATTAATTCATATCTAATTTTAAAGATG-AGTCTTGGCAAAATTAAGGCT 59  
 790 CAAAGATTAATTCATATCTAATTTTAAAGATG-AGTCTTGGCAAAATTAAGGCT 731  
 60 TGGATTAATTCATATCTAATTTTAAAGATG-AGTCTTGGCAAAATTAAGGCT 119  
 730 TGGATTAATTCATATCTAATTTTAAAGATG-AGTCTTGGCAAAATTAAGGCT 671  
 120 GTATTCACA-----CAATCATTCTTCTGATAC---ACTCTGACCAT 163  
 670 GTATTCACA-----CAATCATTCTTCTGATAC---ACTCTGACCAT 611  
 164 TGGAGCTTAATTCATATCTAATTTTAAAGATG-AGTCTTGGCAAAATTAAGGCT 222  
 610 CTGAAATCTTGGCTTCTAATGCTTTGTACAAAGAGATGATGATGATGATGATGATG 551  
 223 TGGATTAATTCATATCTAATTTTAAAGATG-AGTCTTGGCAAAATTAAGGCT 282  
 550 TTTTGGAGCCATATTAACATCTTATGTTTCTTCTTATATGTTTCTGATATTTCC 491  
 283 TGTTCAGGTACCATGTTTCTAATTTTAAAGATG-AGTCTTGGCAAAATTAAGGCT 342  
 490 ATTTTCAAGTACCATGTTTCTAATTTTAAAGATG-AGTCTTGGCAAAATTAAGGCT 431  
 343 GACTTAATTCCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 402  
 430 GACCTAAATATTAATTAAGATTAAGGATGATGATGATGATGATGATGATGATGATGAT 371  
 403 GTTCAATAGTA 413  
 370 GTTCAATAGTA 360

RESULT 3

AL812818 standard; mRNA; EST; 527 BP.

AL812818; AL812818.1  
05-JUL-2002 (Rel. 72, Created)  
02-SEP-2002 (Rel. 72, Last updated, Version 2)  
Triticum aestivum (mercia) clone E03 e411\_plate\_3 maternal tissue (minus endosperm and embryo) 6 days post anthesis  
EST; expressed sequence tag.  
Triticum aestivum (bread wheat)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Triticum.  
[1]  
Wilson I., Beswick R., Shepherd S., Barker G., Parker J., Owen P., Edwards D., Coghill J., Holdsworth W., Denton J., Shewry P., Edwards K.;  
"A BSRRC-funded wheat EST resource for the academic community";  
Unpublished.  
[2]  
1-527  
Barker G.;  
Submitted (03-JUL-2002) to the EMBL/GenBank/DBJ databases.  
Barker G., Institute of Arable Crop Research, Long Ashton, Bristol BS41 9AF  
United Kingdom.

Key Location/Qualifiers  
1. 527  
/db\_xref="taxon:4565"  
/mol\_type="mRNA"  
/organism="Triticum aestivum"  
/cultivar="mercia"  
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Sequence 527 BP; 133 A; 95 C; 125 G; 173 T; 1 other;  
Query Match 6.8%; Score 140; DB 6; Length 527;  
Best Local Similarity 71.9%; Pred. No. 7.8e-17;  
Matches 241; Conservative 0; Mismatches 6; Indels 88; Gaps 1;

1383 AGTCATTCGTAATAATATACCTTGAACGGTTGATGCTTGGATGGCACTGATACAT 1442  
173 AGTCATTCGTAATAATATACCTTGAACGGTTGATGCTTGGATGGCACTGATACAT 232  
1443 TACTTCCACGGTGGCCACGGCCATCATTTGGATGGGATTCCTGCTATTCACATAT 1502  
233 TACTTCCACGGTGGCCACGGCCATCATTTGGATGGGATTCCTGCTATTCACATAT 292  
1503 GGGAGTTGGGAAGTATGATCTGTGACTTCTGTACCATATTTGGCTAACTGTTCTGTT 1562  
293 NGGAGTTGGGAAGT----- 306  
1563 AATCTGTTCTTACACATGTTGATTTCTTATTCAGATTTAGATTTCTTACTGTC 1622  
307 -----ATTAGATTTCTTACTGTC 324  
1623 AAACCGGATGGTGGCTTGAAGATATATAGTTTGATGGATTTGATGGGGTGAC 1682  
325 AAACCGGATGGTGGCTTGAAGATATATAGTTTGATGGATTTGATGGGGTGAC 384  
1683 CTCGATGATGATTACTCAACATGATGATTAACAAGTAA 1717

Db 385 CTCGATGATGATTACTCAACATGATGATTAACAAGTAA 419

RESULT 4  
LOCUS BU972445 476 bp mRNA linear EST 22-OCT-2002  
DEFINITION HB21K16 BC Hordeum vulgare subsp. vulgare cDNA clone HB21K16  
5-PRIME, mRNA sequence.  
ACCESSION BU972445  
VERSION BU972445.1 GI:24223238  
KEYWORDS EST  
SOURCE Hordeum vulgare subsp. vulgare  
ORGANISM Hordeum vulgare subsp. vulgare  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Hordeum.  
1 (bases 1 to 476)

REFERENCE  
AUTHORS Radchuk, V., Zhang, H., Weschke, W., Potokina, E. and Wobus, U.  
TITLE Unpublished (2002)  
JOURNAL  
COMMENT Molecular Markers Group, Department Genbank  
Institute of Plant Genetics and Crop Plant Research (IPK)  
Corrensstr. 3, 06466, Gatersleben, Germany  
Tel: 039482-5522  
Fax: 039482-5595  
Email: stein@ipk-gatersleben.de  
Insert Length: 476 Std Error: 0.00  
Plates: 21 row: X column: 16  
Seq primer: M13rev.

FEATURES  
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/clone\_id="BC"  
/note="Vector: pBluescript SK+; site 1: EcoRI (5'-end of cDNA); site 2: XhoI (3'-end of cDNA); developing caryopsis, 8-15 DAP (days after pollination) Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI).  
NOTE: Also due to the cloning system used, Blue/white selection for recombinants is not 100% reliable."

ORIGIN  
Query Match 6.8%; Score 139.4; DB 13; Length 476;  
Best Local Similarity 71.9%; Pred. No. 1e-16;  
Matches 241; Conservative 0; Mismatches 6; Indels 88; Gaps 1;

1383 AGTCATTCGTAATAATATACCTTGAACGGTTGATGCTTGGATGGCACTGATACAT 1442  
68 AGTCATTCGTAATAATATACCTTGAACGGTTGATGCTTGGATGGCACTGATACAT 127  
1443 TACTTCCACGGTGGCCACGGCCATCATTTGGATGGGATTCCTGCTATTCACATAT 1502  
128 TACTTCCACGGTGGCCACGGCCATCATTTGGATGGGATTCCTGCTATTCACATAT 187  
1503 GGGAGTTGGGAAGTATGATCTGTGACTTCTGTACCATATTTGGCTAACTGTTCTGTT 1562  
188 GGGAGTTGGGAAGT----- 199  
1563 AATCTGTTCTTACACATGTTGATTTCTTATTCAGATTTAGATTTCTTACTGTC 1622

Db 200 -----GTATTAATCTTCTACTGTG 219  
 QY 1623 AAACGCAGATGCTGGGCTTGAGAAATATAAGTTTGATGATTTTCGATTGTGATGGGGTAC 1682  
 Db 220 AAACGCAGATGCTGGGCTTGAGAAATATAAGTTTGATGATTTTCGATTGTGATGGGGTAC 279  
 QY 1683 CTCGATGATGTAATCTACCACTGGATTCACAGTAA 1717  
 Db 280 TTCATGATGTAATCTACCACTGGATTCACAGTAA 314

RESULT	5
LOCUS	BU967331
DEFINITION	BU967331
ACCESSION	H803P08
VERSION	BC Hordeum vulgare subsp. vulgare CDNA clone H803P08
KEYWORDS	5-PRIME, mRNA sequence.
SOURCE	BU967331 GI:24218124
ORGANISM	EST.
	Hordeum vulgare subsp. vulgare
	Hordeum vulgare subsp. vulgare
	Euxaropta, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
	Pooideae; Triticeae; Hordeum.
REFERENCE	1 (bases 1 to 537)
AUTHORS	Radchuk, V., Zhang, H., Weschke, W., Potokina, E. and Wobus, U.
TITLE	Barley ESTs from developing seeds
JOURNAL	Unpublished (2002)
COMMENT	Contact: Stejn Nils Molecular Markers Group, Department Genbank Institute of Plant Genetics and Crop Plant Research (IPK) Corrensstr. 3, 06466, Gatersleben, Germany Tel.: 039482-5522 Fax: 039482-5595 Email: stein@ipk-gatersleben.de Insert length: 537 Std Error: 0.00 Plate: 3 row; P column: 8 Seq primer: M13rev.

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FEATURES
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                /dev_stage="8-15 DAP (days after pollination)"
                /lab_host="X110-Gold"
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                cDNA); Site 2: XhoI (3'-end of cDNA)-developing
                caryopsis, 8-15 DAP(days after pollination) due to a
                cloning artefact caused by the kit, in most cases the
                EcoRI site is NOT present, as well as the EcoRIadapter
                used for cloning. To excise the insert, restriction sites
                upstream EcoRI should be used (e.g. BamHI, SalI, PstI).
                NOTE: Also due to the cloning system used Blue/White
                selection for recombinants is not 100% reliable."

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ORIGIN	Query Match	Best Local Similarity	Score	DB	Length
Matches	241;	Conservative	0;	Mismatches	6;
				Indels	88;
				Gaps	1
QY	1383	AGTCATTGCTCAATATATATACCTTGAAGGTTTAAATGCTTCATGCACTGATATACAT	144		
DB	29	AGTCATTGCTCAATATATATACCTTGAAGGTTTAAATGCTTCATGCACTGATATACAT	88		
QY	1443	TACTTCCAGAGTGATCCACGCGGCCATTCATTTGATGTGGATTTCTGCTATTTCACATAT	156		
DB	89	TACTTCCAGAGTGATCCACGCGGCCATTCATTTGATGTGGATTTCTGCTATTTCACATAT	148		

QY	1503	GGAGATTGGGAAGATGATGACTCTGCAATTTGACACAAATTTGGCTAACGTTCCAGTT	1562
	149	GGAGATTGGGA-----	160
Db	1563	AATCTGTTCTTACACAGATGATATCTATCTTATGACAGATATTGACATTTCTACTGTC	1622
QY	161	-----GATTTAAGATCTTACGTC	180
Db	1623	AAACGCCAGATGCGGCTTGAAAGATATAAGCTTGATGATTCGATTTGTGGGGTGAC	1682
QY	181	AAACGCCAGATGGGGCTTAAAGAAATTAAGTTTGATGAGATTTGATTTTGAATGGGGTGAC	240
Db	1683	CTCCATGATGATATCTACCATGGATTTCAAGTAA	1717
QY	241	TTCCATGATGATATCTACCATGGATTTCAAAATGA	275
Db			

RESULT 6  
BQ245037  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BQ245037  
TAE150332A02R  
sequence.  
BQ245037  
BQ245037.1  
GI:20440913  
EST.  
Triticum aestivum (bread wheat)  
Triticum aestivum  
Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Triticum.  
1 (bases 1 to 476)  
Cloutier, S.  
Wheat functional genomics - Genlea developing seeds cDNA libraries unpublished (2002)  
Contact: Dr. Sylvie Cloutier  
Genetic Engineering and Agri-Food Canada

476 bp  
mrna  
linear  
EST 03-MAY-2002  
TAE150332A02R, mrna

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ORIGIN	Query Match	6.5%	Score 134	DB 13	Length 476
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Db	142	TTACAAAGACCTTACTGCGAACAATGCGCAATATTTTGGATTGGCTACTGATGTTGAT	201		
QY	1969	GCGGTAGTTACTGATGCTGGTCAACGATCTTAATTCATGAGCTTTATCCTGATGCTGTA	202		
Db	202	GCGGTGCTTTAATTGATGCTGGTCAACGATCTTAATTCATGAGCTTTATCCTGATGCTGTA	261		

QY 2029 TCACATGTTGAGATGTAGT 2050  
DB 262 TCACATGTTGAGATGTAGT 283

RESULT 7  
LOCUS BU986646  
DEFINITION HF12102r HF Hordeum vulgare subsp. vulgare cDNA clone HF12102  
ACCESSION BU986646 623 bp mRNA linear EST 22-OCT-2002  
VERSION BU986646  
KEYWORDS 5-PRIME, mRNA sequence.  
SOURCE BU986646.1 GI:24237592  
ORGANISM Hordeum vulgare subsp. vulgare  
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Hordeum.  
REFERENCE 1 (bases 1 to 623)  
AUTHORS Radchuk, V., Zhang, H., Weschke, W., Potokina, E. and Mabus, U.  
TITLE Barley ESTs from developing seeds  
JOURNAL Unpublished (2002)  
COMMENT Contact: Stein Nils  
Molecular Markers Group, Department Genbank  
Institute of Plant Genetics and Crop Plant Research (IPK)  
Corrensstr. 3, 06466, Gatersleben, Germany  
Tel: 039482-5522  
Fax: 039482-5595  
Email: stein@ipk-gatersleben.de  
Insert Length: 623 Std Error: 0.00  
Plate: 12 row: 1 column: 2  
Seq primer: M13rev.  
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/lab\_host="XL10-Gold"  
/clone\_lib="HF"  
/note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of cDNA); Site 2: XhoI (3'-end of cDNA); developing caryopsis, 16-25 DAF (days after flowering) Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinants is not 100% reliable. Average insert size is 940 bp"

ORIGIN  
Query Match 6.5%; Score 134; DB 13; Length 623;  
Best Local Similarity 96.5%; Pred. No. 1.1e-15;  
Matches 137; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

DB 1383 AGTCATTCGTCATTAATACCTTGACGGTTGATGTTTCGATGGCACTGATACAT 1442  
DB 463 AGTCATTCGTCATTAATACCTTGACGGTTGATGTTTCGATGGCACTGATACAT 522

QY 1443 TACTTCACAGGTGTCACAGCGGCCCATTCATGATGGATTCGTCATTAAT 1502  
DB 523 TACTTCACAGGTGTCACAGCGGCCCATTCATGATGGATTCGTCATTAAT 582

QY 1503 GGGAGTTGGAGTATGAGT 1524

DB 583 GGGAGTTGGAGTATGAGT 604

RESULT 8  
LOCUS AQ576669/c  
DEFINITION nbxb008901r CUGI Rice BAC Library Oryza sativa (japonica cultivar-group) genomic clone nbxb008901r, genomic survey sequence.  
ACCESSION AQ576669 610 bp DNA linear GSS 02-JUN-1999  
VERSION AQ576669  
KEYWORDS AQ576669.1 GI:4977154  
SOURCE GSS.  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Eriocaridaceae; Oryzaceae; Oryza.  
REFERENCE 1 (bases 1 to 610)  
AUTHORS Wang, R. A. and Dean, R. A.  
TITLE A BAC End Sequencing Framework to Sequence the Rice Genome  
JOURNAL Unpublished (1998)  
COMMENT Contact: Wang RA  
Clemson University Genomics Institute  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 7268  
Fax: 864 656 4293  
Email: twing@clemson.edu  
Seq primer: GGAACAGCTATGACCATG  
Class: BAC ends  
High quality sequence stop: 442.  
Location/Qualifiers  
1..610  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="genomic DNA"  
/strain="japonica"  
/cultivar="Nipponbare"  
/db\_xref="taxon:39947"  
/clone="nbxb008901r"  
/tissue\_type="leaf"  
/lab\_host="E. coli DH10B"  
/clone\_lib="CUGI Rice BAC Library"  
/note="Vector: pBelBAC11; Site 1: HindIII; Site 2: HindIII; Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."

ORIGIN  
Query Match 6.5%; Score 133.2; DB 28; Length 610;  
Best Local Similarity 59.1%; Pred. No. 1.5e-15;  
Matches 344; Conservative 0; Mismatches 168; Indels 70; Gaps 4;

QY 1478 GTGGAGTTTCGTCATTAATACCTTGAGTTGGAGTTGGAGTA-----TGTAGCTCTGA 1528  
DB 610 GTGGAGTTTCGTCATTAATACCTTGAGTTGGAGTTGGAGTAAGAACACCTTAATCCTCT 551

QY 1529 CTTCTGCACCATATTGGCTAACTGTTCTTATATCTGTTCTTAACACATGTTGATATT 1588

	Best local similarity	95.8%	Pred No.	2,2e-15;	Mismatches	6;	Indels	0;	Gaps	0;
	Matches	133;	Conservative	0;						
QY	1909	TTCAGATGACATTACTTCTGGGAACAATAATCGCAAAATTTTGCAATTTGTCTACTGATGTTGAT	1968							
Dd	96	TTCAAAATGACATTTAATCTGCGAAGTAATGAGCATATTTTTGAAVTTGGTACTGATGTTGAT	155							
QY	1569	GCGGTACTTACTTGATGATGCCTGCGAACGATCCTATATCATGAGCACTTATCCMGANCGCTGA	2028							
Dd	156	GCGGTACTTACTTGATGATGCCTGCGAACGATCCTATATCATGAGCACTTATCCMGATGCTGA	215							
OY	2029	TCGATTGGTAGAGATGATGATG	2050							
Dd	216	TCGATTGGTAGAGATGATGATG	237							
RESULT	10									
LOCUS	AV939010	678 bp	mRNA	linear	EST 18-JAN-2002					
DEFINITION	AV939010 K. Sato unpublished cDNA library; strain H602 adult,									
	heading stage top three leaves Hordeum vulgare subsp. spontaneum									
	cDNA clone dah20e24 5' , mRNA sequence.									
ACCESSION	AV939010									
VERSION	AV939010.1	GI:18234807								
KEYWORDS	EST.									
SOURCE	Hordeum vulgare subsp. spontaneum									
ORGANISM	Hordeum vulgare subsp. spontaneum									
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;									
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;									
	Pooidae; Triticeae; Hordeum.									
	1 (bases 1 to 678)									
REFERENCE	Sato, K., Saisho, D. and Takeda, K.									
AUTHORS	Barley EST sequencing project in NIG and Okayama Univ									
JOURNAL	Unpublished (2002)									
COMMENT	Contact: Tadasu Shin-i Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel.: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshini@genie.nig.ac.jp. Location/Qualifiers									
FEATURES										
source	1..678									
	/organism="Hordeum vulgare subsp. spontaneum"									
	/mol_type="mRNA"									
	/strain="H602"									
	/sub_species="spontaneum"									
	/db_xref="taxon:77009"									
	/clone="dah20e24"									
	/tissue_type="top three leaves"									
	/dev_stage="adult, heading stage"									
	/clone_1lb="K. Sato unpublished cDNA library, strain H602									
	adult, heading stage top three leaves"									
ORIGIN										
Query Match	6.1%; Score 125.8; DB 9; Length 678;									
Best Local Similarity	84.0%; Pred. No. 3.9e-14;									
Matches 142; Conservative	0; Mismatches 27; Indels 0; Gaps 0;									
X	280 GCCTGTTCACGAGACCAGTGTACTAATTTTTTGCACACCAAGTACGCCGTTTGGAACTCCA	339								



BUN70967 411 bp mRNA linear EST 22-OCT-2002  
 LOCUS Hb16D15r BC Hordeum vulgare subsp. vulgare cDNA clone Hb16D15  
 DEFINITION 5-PRIME, mRNA sequence.  
 ACCESSION BUN70967  
 VERSION BUN70967.1 GI:24221760  
 KEYWORDS EST.  
 SOURCE Hordeum vulgare subsp. vulgare  
 ORGANISM Hordeum vulgare subsp. vulgare  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Poideae; Triticeae; Hordeum.  
 REFERENCE 1 (bases 1 to 411)  
 AUTHORS Radchuk, V., Zhang, H., Wesschke, W., Potokina, E. and Wobus, U.  
 TITLE Barley ESTs from developing seeds  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Stein Nils  
 Molecular Markers Group, Department Genbank  
 Institute of Plant Genetics and Crop Plant Research (IPK)  
 Corrensstr. 3, 06466, Gatersleben, Germany  
 Tel: 039482-5522  
 Fax: 039482-5595  
 Email: stein@ipk-gatersleben.de  
 Insert Length: 411 Std Error: 0.00  
 Plate: 16 row: D column: 15  
 Seq primer: M13rev.  
 Location/Qualifiers  
 1..411  
 /organism="Hordeum vulgare subsp. vulgare"  
 /mol\_type="mRNA"  
 /cultiVar="barke"  
 /sub\_species="vulgare"  
 /db\_xref="GABI:235798"  
 /db\_xref="taxon:112509"  
 /clone="Hb16D15"  
 /issue\_type="developing caryopsis"  
 /dev\_stage="8-15 DAP (days after pollination)"  
 /lab\_host="XL10-Gold"  
 /clone\_1b="BC"  
 /note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of cDNA); Site 2: XhoI (3'-end of cDNA); developing caryopsis, 8-15 DAP (days after pollination) Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI).  
 NOTE: Also due to the cloning system used Blue/White selection for recombinants is not 100% reliable."

VERSION CA292638.1 GI:36051621  
 KEYWORDS EST.  
 SOURCE Saccharum officinarum  
 ORGANISM Saccharum officinarum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCB  
 clade; Panicoidae; Andropogonaceae; Saccharum.  
 REFERENCE 1 (bases 1 to 618)  
 AUTHORS Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.  
 TITLE The libraries that made SUCEST  
 JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)  
 COMMENT Contact: Arruda P  
 Centro de Biologia Molecular e Engenharia Genetica  
 Universidade Estadual de Campinas  
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
 Tel: 55 19 3788 1137  
 Fax: 55 19 3788 1089  
 Email: parruda@unicamp.br  
 Clone distribution: clone distribution information can be found  
 through the Brazilian Clone Collection Center (BCCC) at  
 http://www.bcccenter.fcav.unesp.br  
 Plate: 025 row: G column: 06  
 Seq primer: T7 Promoter Primer.  
 Location/Qualifiers  
 1..618  
 /organism="Saccharum officinarum"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:4547"  
 /clone="SCRF1027B04"  
 /lab\_host="DH10B"  
 /clone\_1b="FL8"  
 /note="Organ: Developing inflorescence and rachis (10cm-long); Vector: pSPori; Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from [developing inflorescence and rachis (10cm-long)]. cDNA was prepared from polyA+ mRNA using Superscript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sapharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at  
 http://succest.lad.lic.unicamp.br/public"

ORIGIN  
 Query Match 6.1%; Score 124.4; DB 13; Length 411;  
 Best Local Similarity 92.3%; Pred. No. 8.1e-14;  
 Matches 131; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

ORIGIN  
 Query Match 6.0%; Score 123.2; DB 14; Length 618;  
 Best Local Similarity 91.0%; Pred. No. 1.3e-13;  
 Matches 131; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Db 144 TTACAAATGACATTACTGCGAACAATGCGGATTTGGATTCGCCACTGATGTTGAT 203  
 1909 TTCTAGATGACATTACTGCGAACAATGCGGATTTGGATTTGCTACTAGTGTGAT 1968  
 QY 1969 GCGGAGTTTACTGATGTCGTCACGATCTAATTCATGAGCTTATCCTGATGCTGA 2028  
 Db 204 GCGGAGTTTACTGATGTCGTCACGATCTAATTCATGAGCTTATCCTGATGCTGA 263  
 QY 2029 TCCATTGGTGAAGATGTAAGTG 2050  
 Db 264 TCCATTGGTGAAGATGTCAGCG 265

Db 1383 AGTATTCGCAATTAATACCTTGACGCTTGAATGTTGGATGGACGACATACACAT 1442  
 Db 218 AGTATTCGCAATTAATACCTTGACGCTTGAATGTTGGATGGACATACACAT 277  
 QY 1443 TACTTCACGAGTGTTCACGCGGCATCATGATGATGAGATTCTGCTATTCACATAT 1502  
 Db 278 TACTTCATGATGTTCCACGCGGCATCATGATGATGAGATTCTGCTATTCACATAT 337  
 QY 1503 GCGAGTTGGGAAGTATGATGCTCT 1526  
 Db 338 GCGAGTTGGGAAGTATGATGATAT 361

RESULT 12 CA292638 618 bp mRNA linear EST 26-SEP-2003  
 LOCUS SCRF1027B04.g FL1 Saccharum officinarum cDNA clone SCRF1027B04  
 DEFINITION 5', mRNA sequence.

RESULT 13 CA202517 650 bp mRNA linear EST 25-SEP-2003  
 LOCUS SCRF1027B04.g FL1 Saccharum officinarum cDNA clone SCRF1027B04  
 DEFINITION 5', mRNA sequence.

DEFINITION 5', mRNA sequence.

DEFINITION 5', mRNA sequence.

REFERENCE 1 (bases 1 to 650)  
 AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.  
 TITLE The libraries that made SUCEST  
 JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)  
 COMMENT Centro de Biologia Molecular e Engenharia Genetica  
 Universidade Estadual de Campinas  
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
 Tel: 55 19 3788 1137  
 Fax: 55 19 3788 1089  
 Email: parud@unicamp.br  
 Location/Qualifiers  
 source  
 FEATURES  
 1..650  
 /organism="Saccharum officinarum"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:4547"  
 /clone="SCRFPL027804"  
 /lab\_host="DH10B"  
 /clone\_lib="FL1"  
 /note="Organ: Inflorescence at beginning of development (1cm-long); Vector: pSPORT1; Site\_1: SalI; Site\_2: NotI; An unidirectional cDNA library generated from Inflorescence at beginning of development (1cm-long). cDNA was prepared from polyA+ mRNA using Superscript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.1ad.1c.unicamp.br/public"

ORIGIN  
 Query Match 6.0%; Score 123.2; DB 14; Length 650;  
 Best Local Similarity 91.0%; Pred. No. 1.2e-13;  
 Matches 131; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1383 AGTCATTCGCAAAATTAATACCCCTTGACGCTTGGAATGGTTCGATGGACATGATACAT 1442  
 DB 188 AGTCATGATCAAAATTAATACCTTGAGCGGTTGAATGGTTCGATGGACATGATACAT 247  
 QY 1443 TACTTCCAGCGGTGTCACGCGGCATCATGATGGATTCGCTCATTCGAACAT 1502  
 DB 248 TACTTCCATGATGATCCACGCGGCATCATGATGGATTCGCTCATTCGAATAT 307  
 QY 1503 GGGAGTTGGAGATGATGACTCT 1526  
 DB 308 GGGAGTTGGAGATGATGACTAT 331

RESULT 14  
 AY109521 2766 bp mRNA linear HTC 17-OCT-2002  
 LOCUS AY109521  
 DEFINITION Zea mays CL1245\_1 mRNA sequence.  
 ACCESSION AY109521  
 VERSION AY109521.1 GI:21213273  
 KEYWORDS HTC.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 Zea mays  
 Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.  
 Maize Mapping Project/Dupont Consensus Sequences for Design of Overgo Probes  
 JOURNAL Unpublished (2002)

REFERENCE 2 (bases 1 to 2766)  
 AUTHORS Coe,E.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (25-Apr-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA  
 COMMENT If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSU, maizegap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.  
 Location/Qualifiers  
 source  
 FEATURES  
 1..2766  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:4577"  
 /db\_xref="ZmDB:630161"  
 /clone\_lib="Maize Mapping Project/Dupont Consensus Library"  
 /note="This sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont contigs; this resource was assembled by Dupont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

ORIGIN  
 Query Match 6.0%; Score 122.2; DB 11; Length 2766;  
 Best Local Similarity 88.1%; Pred. No. 1.4e-13;  
 Matches 133; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1393 AGTCATTCGCAAAATTAATACCCCTTGACGCTTGGAATGGTTCGATGGACATGATACAT 1442  
 DB 1172 AGTCATTCATCAAAATTAATACCTTGATGGTTCGAATGGTTCGATGGACATGATACAT 1231  
 QY 1443 TACTTCCAGCGGTGTCACGCGGCATCATGATGGATTCGCTCATTCGAACAT 1502  
 DB 1232 TACTTCCATGATGATCCACGCGGCATCATGATGGATTCGCTCATTCGAATAT 1291  
 QY 1503 GGGAGTTGGAGATGATGACTCTGACTTCT 1533  
 DB 1292 GGGAGTTGGAGATGATGACTTCTATGAT 1322

RESULT 15  
 BM660711 399 bp mRNA linear EST 27-FEB-2002  
 LOCUS BM660711  
 DEFINITION 952041807.xl 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea mays cDNA, mRNA sequence.  
 ACCESSION BM660711  
 VERSION BM660711.1 GI:18963932  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 Zea mays  
 Walbot,V.  
 Maize ESTs from various cDNA libraries sequenced at Stanford University  
 Unpublished (1999)  
 CONTACT Walbot V  
 JOURNAL Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Plate: 952041 row: B column: 07.  
 Location/Qualifiers  
 source  
 1..399

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/organism="Zea mays"
/mol_type="mRNA"
/cultivar="BMS (Black Mexican Sweet)"
/db_xref="taxon:4577"
/tissue_type="suspension culture"
/dev_stage="mixed logarithmic and stationary growth
phases"
/lab_host="DH103"
/clone_id="952 - BMS tissue from Walbot lab (reduced
rRNA)"
/note="Vector: pUC19; Site 1: EcoRI; Site 2: EcoRI; The
library was prepared by George Rudenko using poly (A)
selected RNA and Universal Riboclone cDNA Synthesis System
(Promega). cDNA was synthesized using both random and
oligo(dT) primers in separate reactions and equipped with
EcoRI adaptors. Library was size-fractionated on agarose
gels (for insert size >400bp) and non-directionally cloned
into EcoRI-digested pUC19 vector. Blue/white selection on
carbenicillin-containing plates was used to recover
positive clones."

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## ORIGIN

```

Query Match      5.9%; Score 121.6; DB 12; Length 399;
Best Local Similarity 82.7%; Pred. No. 2.8e-13;
Matches 139; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 1383 AGTCATTGTCGAATATATACCCCTTGACGGTTGAATGATTGCGATGGCACTGATACACAT 1442
    |||||
DB 224 AGTCATTGTCGAATATATACCCCTTGATGTTGAATGATTGATGGCACTGATACACAT 283
    |||||

QY 1443 TACTTCCACGGTGGTCCACGGCCCATCTTGATGTGGGATTTCTGCTATTCACATAT 1502
    |||||
DB 284 TACTTCCATGGGTGCCACGGGCCCATCTTGATGTGGGATTTCTGCTATTCACATATAT 343
    |||||

QY 1503 GGGAGTTGGGAAGTATGTAGCTGTGACTTCTGTCAACCATATTTGGCTA 1550
    |||||
DB 344 GGGAGTTGGGAAGTTTGAAGATTTCTACTGTCAATGCGAGATGGCGA 391
    |||||

```

Search completed: April 10, 2004, 14:06:33  
 Job time : 5423.32 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 10, 2004, 01:54:35 ; Search time 5268.31 seconds

(without alignments)  
11057.263 Million cell updates/sec

Title: US-09-508-377-10\_COPY\_10120\_11463

Perfect score: 1344

Sequence: 1 ttgataatcgcggtatcgca.....tcgctcaacgtaaatcc 1344

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_hcg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_scs:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vt:\*  
15: gb\_wa:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_scs:\*  
28: em\_un:\*  
29: em\_vt:\*  
30: em\_hcg\_hum:\*  
31: em\_hcg\_inv:\*  
32: em\_hcg\_other:\*  
33: em\_hcg\_mus:\*  
34: em\_hcg\_pln:\*  
35: em\_hcg\_rtd:\*  
36: em\_hcg\_mam:\*  
37: em\_hcg\_vrt:\*  
38: em\_sy:\*  
39: em\_hcg\_hum:\*  
40: em\_hcg\_mus:\*  
41: em\_hcg\_other:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	1344	100.0	11463	6 AX031271
2	1344	100.0	11475	8 AF38431
3	370	27.5	1119	6 AX756279
4	370	27.5	2853	6 AR340173
5	370	27.5	2853	6 TA06376
6	361.6	26.9	2970	8 AF286319
7	360.6	26.8	2726	8 AF38432
8	360	26.8	2970	8 TASB2
9	263.6	19.6	2554	8 AF064560
10	158.8	11.8	2549	8 BT008928
11	132.4	9.9	1292	8 AY235404
12	132.4	9.9	1373	8 AY235395
13	132.4	9.9	1374	8 AY235421
14	132.4	9.9	1382	8 AY235405
15	132.4	9.9	1393	8 AY235396
16	132.4	9.9	1393	8 AY235399
17	132.4	9.9	1394	8 AY235397
18	132.4	9.9	1394	8 AY235407
19	132.4	9.9	1394	8 AY235409
20	132.4	9.9	1394	8 AY235410
21	132.4	9.9	1394	8 AY235415
22	132.4	9.9	1397	8 AY235394
23	132.4	9.9	1399	8 AY235398
24	132.4	9.9	1399	8 AY235408
25	132.4	9.9	1399	8 AY235416
26	132.4	9.9	1399	8 AY235418
27	132.4	9.9	1399	8 AY235419
28	132.4	9.9	1399	8 AY235422
29	132.4	9.9	1400	8 AY235400
30	132.4	9.9	1400	8 AY235401
31	132.4	9.9	1400	8 AY235402
32	132.4	9.9	1400	8 AY235403
33	132.4	9.9	1400	8 AY235411
34	132.4	9.9	1400	8 AY235412
35	132.4	9.9	1400	8 AY235413
36	132.4	9.9	1400	8 AY235414
37	132.4	9.9	1400	8 AY235420
38	132.4	9.9	1401	8 AY235417
39	132.4	9.9	1618	8 AF235406
40	132.4	9.9	23449	8 AF072725
41	125.6	9.3	2446	6 AR427891
42	125.6	9.3	2795	8 ZMU65948
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45	123.4	9.2	2364	6 E14724

## ALIGNMENTS

RESULT 1  
AX031271 11463 bp DNA linear PAT 20-SHP-2000  
LOCUS  
DEFINITION Sequence 10 from Patent WO9914314.  
ACCESSION AX031271  
VERSION AX031271.1 GI:10278603  
KEYWORDS  
SOURCE  
ORGANISM  
Aegilops tauschii  
Aegilops tauschii  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Aegilops.  
REFERENCE  
1 Li, Z., Morell, M. and Rahman, S.  
Regulation of gene expression in plants  
TITLE

JOURNAL Patent: WO 9914314-A 10 25-MAR-1999;  
GOODMAN FIDLER LTD (AU) ; LI ZHONGYI (AU) ; MORELL MATTHEW (AU) ;  
RAHMAN SADIQUR (AU) ; UNIV AUSTRALIAN (AU) ; COMM SCIENT IND RES  
ORG (AU) ; GROUPE LIMAGRAIN PACIFIC PTY L (AU)  
Location/Qualifiers  
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ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGATATATCGTGTATGCAAGAGTTCATCGACGCAATGCGACATCTTGAGAAAAATATG 60  
DB 10120 TTGATATATCGTGTATGCAAGAGTTCATCGACGCAATGCGACATCTTGAGAAAAATATG 10179  
QY 61 GGGTATGTCATCGTGTATGCTTTGTCATPACAAAGTCACAGTTAAAGTACGTCCTC 120  
DB 10180 GGGTATGTCATCGTGTATGCTTTGTCATPACAAAGTCACAGTTAAAGTACGTCCTC 10239  
QY 121 AAGTGTAAAAAAGTGTAGATTAATTCCTGTANTGATGATAAAGTGTGCAAGGCG 180  
DB 10240 AAGTGTAAAAAAGTGTAGATTAATTCCTGTANTGATGATAAAGTGTGCAAGGCG 10299  
QY 181 AGCTGGAATGCTTTTACCAAAAAGTATTTCTTAAGTCTGTGTATGATACATATAC 240  
DB 10300 AGCTGGAATGCTTTTACCAAAAAGTATTTCTTAAGTCTGTGTATGATACATATAC 10359  
QY 241 CAGACATGACAATGTACTGCAAGTTATGACATGTCAGACCAATGATGTTCAAGGAAC 300  
DB 10360 CAGACATGACAATGTACTGCAAGTTATGACATGTCAGACCAATGATGTTCAAGGAAC 10419  
QY 301 ATGAGAGAGATTAAGTATCATCTCTCAAAAAGAGAGATTTGGTATTTGTTCAACTTC 360  
DB 10420 ATGAGAGAGATTAAGTATCATCTCTCAAAAAGAGAGATTTGGTATTTGTTCAACTTC 10479  
QY 361 ACTGAGACAATAGCTTTTGTGACTACCGTGTGGGTGTTCCAAAGCTTGGAAATCAAG 420  
DB 10480 ACTGAGACAATAGCTTTTGTGACTACCGTGTGGGTGTTCCAAAGCTTGGAAATCAAG 10539  
QY 421 TAGGCTTGCTTTTCAATGTCACCCCTTCAACAGTAAAGGTTAGGGGGCTTCTCAACT 480  
DB 10540 TAGGCTTGCTTTTCAATGTCACCCCTTCAACAGTAAAGGTTAGGGGGCTTCTCAACT 10599  
QY 481 TTAAATTCACATGATAGATTTGTTGATGTCAGCTATCAATATTAAGATAGAGTA 540  
DB 10600 TTAAATTCACATGATAGATTTGTTGATGTCAGCTATCAATATTAAGATAGAGTA 10659  
QY 541 ATTGTGAAGAAAAAATTGCTGAGCTGTGTAGCCATGGAAGGTGTTCTTAAACAG 600  
DB 10660 ATTGTGAAGAAAAAATTGCTGAGCTGTGTAGCCATGGAAGGTGTTCTTAAACAG 10719  
QY 601 CCGCGAAGCACAATACATCATATTAATCTAAGTAAAGTGTGTTCAATCTTTATG 660  
DB 10720 CCGCGAAGCACAATACATCATATTAATCTAAGTAAAGTGTGTTCAATCTTTATG 10779  
QY 661 CTCAGTTGAGCTGGTCTAATACAGACTATTTCCGAATCTACCCATACCATCTTAC 720  
DB 10780 CTCAGTTGAGCTGGTCTAATACAGACTATTTCCGAATCTACCCATACCATCTTAC 10839  
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DB 10840 AGTTTATGAGACGCCCATTTTGAACAATGCTGGGTTTGTATGTTGTGACAGTTTCT 10899  
QY 781 GCATTTCTTAATAGGTGGCTTGGACTCTGAGATGCACTCTTGGTGAATTCAGAG 840

DB 10900 GCATTTCTTAATAGGTGGCTTGGACTCTGAGATGCACTCTTGGTGAATTCAGAG 10959  
QY 841 GCTTGATCATGATGTCGACTACTTACAAACGCTAAGTCTGAGCTCAAGGTCATCTGACT 900  
DB 10960 GCTTGATCATGATGTCGACTACTTACAAACGCTAAGTCTGAGCTCAAGGTCATCTGACT 11019  
QY 901 GCTCTTGACTCAACGCTCTTACAAATCTGAATCACTCCCATTTGCTGATGGCTTGACG 960  
DB 11020 GCTCTTGACTCAACGCTCTTACAAATCTGAATCACTCCCATTTGCTGATGGCTTGACG 11079  
QY 961 GAACATCCGCAATGACAACAGCGCGCTCTTTCTGAGTATACCTCCGACAGAACTGCG 1020  
DB 11080 GAACATCCGCAATGACAACAGCGCGCTCTTTCTGAGTATACCTCCGACAGAACTGCG 11139  
QY 1021 GTGCTGTATGCCCTTACAGATTAAGAACCCAGACGCGCTTGTATCAAGGCAAGAGAA 1080  
DB 11140 GTGCTGTATGCCCTTACAGATTAAGAACCCAGACGCGCTTGTATCAAGGCAAGAGAA 11199  
QY 1081 CTCACAGAGAGCTCGTGAATCGTGAAGGAGACGACGCGGCAACGCGGAGGCTCTCCAG 1140  
DB 11200 CTCACAGAGAGCTCGTGAATCGTGAAGGAGACGACGCGGCAACGCGGAGGCTCTCCAG 11259  
QY 1141 CGCCATGACTGGGAGGAGATCGTCTCTTCCCAAGATCCAGAGAGAGAGATGATAG 1200  
DB 11260 CGCCATGACTGGGAGGAGATCGTCTCTTCCCAAGATCCAGAGAGAGAGATGATAG 11319  
QY 1201 GTAGCTTGTGTGAGCGCTCGAAGAAATGAGCGGCTGGGTGTTGTTGCTGCA 1260  
DB 11320 GTAGCTTGTGTGAGCGCTCGAAGAAATGAGCGGCTGGGTGTTGTTGCTGCA 11379  
QY 1261 CTGAACCTCCCTCCATCTTGCACATTCGCGGTGTTTGTGACATATCTAATATG 1320  
DB 11380 CTGAACCTCCCTCCATCTTGCACATTCGCGGTGTTTGTGACATATCTAATATG 11439  
QY 1321 CCGGTGCGCTCAAGTGAATAATCC 1344  
DB 11440 CCGGTGCGCTCAAGTGAATAATCC 11463  
RESULT 2  
AF338431 11475 bp DNA linear PLN 27-MAR-2001  
LOCUS Aegilops tauschii starch branching enzyme IIa gene, complete cds.  
DEFINITION  
AF338431  
ACCESSION  
AF338431.1 GI:13447949  
VERSION  
KEYWORDS  
ORGANISM  
Aegilops tauschii  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Pooideae; Triticaceae; Aegilops.  
REFERENCE  
1 (bases 1 to 11475)  
Rahman,S., Regina,A., Li,Z., Sharon,A. and Morell,M.K.  
Kosar-Hashemi,B., Abraham,S. and Morell,M.K.  
Comparison of starch-branching enzyme genes reveals evolutionary  
relationships among isoforms. Characterization of a gene for  
starch-branching enzyme IIa from the wheat genome donor Aegilops  
tauschii  
JOURNAL Plant Physiol. 125 (3), 1314-1324 (2001)  
MEDLINE 21140316  
PUBMED 11244112  
REFERENCE 2 (bases 1 to 11475)  
Rahman,S., Regina,A., Li,Z., Sharon,A. and Morell,M.K.  
Direct Submission  
TITLE  
JOURNAL Submitted (18-JAN-2001) Plant Industry, CSIRO, Clunies Rose,  
Camberra, ACT 2601, Australia  
FEATURES  
source  
1. 11475  
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EXKRIEADIDHGEGLAEFSGYEKLGFTSABGITYREAPGASALVGFENNMP  
NADIMTDYGVWEIPLNNAQSSAIPHSRVKIMDTSGVDSISAMIKESVQAP  
GIPENGIYDDPEEEKYVQHPQRKPESLRIYESHIQMSPEPKINSYANPEVL  
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ORIGIN

Query Match 100.0%; Score 1344; DB 8; Length 11475;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TTGAGATCGTGTATGCAAGAGTTCGATCAGCAATGACATCTTGAGAAAAATATG	60
DB	10132	TTGATATCGTGTATGCAAGAGTTCGATCAGCAATGACATCTTGAGAAAAATATG	10191
QY	61	GGGTATGTCATGCTGTTGCTTTGTTGCATPAACAAGTCACGTTTAACTGATCTCTC	120
DB	10192	GGGTATGTCATGCTGTTGCTTTGTTGCATPAACAAGTCACGTTTAACTGATCTCTC	10251
QY	121	AAGTGTAAAAAAGTGTAAATTAATTCCTGTATGATGAGAAAATGTCGCAAGGCGG	180
DB	10252	AAGTGTAAAAAAGTGTAAATTAATTCCTGTATGATGAGAAAATGTCGCAAGGCGG	10311
QY	181	AGCTGAATGCTTTTACCAAAACATTTTCTTAAGTCTTGATATGATATATAC	240
DB	10312	AGCTGAATGCTTTTACCAAAACATTTTCTTAAGTCTTGATATGATATATAC	10371
QY	241	CAGCACTGACATGTAACTGCAAGTTATGACATGTGACACCAAGTATGTCACGGAAC	300
DB	10372	CAGCACTGACATGTAACTGCAAGTTATGACATGTGACACCAAGTATGTCACGGAAC	10431
QY	301	ATGAGAGAATAGTATGATCTCTCAAAAGAGAGATTGTTGTTTCAACTTC	360
DB	10432	ATGAGAGAATAGTATGATCTCTCAAAAGAGAGATTGTTGTTTCAACTTC	10491
QY	361	ACTGAGACATAGCTTTTGTGACTACCGTGTGGGTGTTCCAAAGCTGGAAGTACAAG	420
DB	10492	ACTGAGACATAGCTTTTGTGACTACCGTGTGGGTGTTCCAAAGCTGGAAGTACAAG	10551
QY	421	TATGCTTGCTTTTCACTGTCACCTTCCACCAAGTGGGTTAGTGGGGCTTTCACACT	480
DB	10552	TATGCTTGCTTTTCACTGTCACCTTCCACCAAGTGGGTTAGTGGGGCTTTCACACT	10611
QY	481	TTTAATTCACATGAGATGTTGTTGTCGCAAGTATCATATATAAGATAGGGTA	540
DB	10612	TTTAATTCACATGAGATGTTGTTGTCGCAAGTATCATATATAAGATAGGGTA	10671
QY	541	ATTGTAAGAAAAAGATTGCTGACCTGTTGTAGCCATAGGAAGTGTCTTTACAG	600

DB	10672	ATTGTAAGAAAAAGATTGCTGACCTGTTGTAGCCATAGGAAGTGTCTTTACAG	10731
QY	601	CCCCGAGACATACCATTCATTCATATATCTAGTGTGTTCAATCTTATG	660
DB	10732	CCCCGAGACATACCATTCATTCATATATCTAGTGTGTTCAATCTTATG	10791
QY	661	CTCAGTTGACCTGGCTTAATCTAGTAACTATTTTCCGATCTACCCCTACCTAGC	720
DB	10792	CTCAGTTGACCTGGCTTAATCTAGTAACTATTTTCCGATCTACCCCTACCTAGC	10851
QY	721	AGTTTAAAGACGCCCATTTGGAACAATGGCTGGGTTTGTAGTTGACAGTTCT	780
DB	10852	AGTTTAAAGACGCCCATTTGGAACAATGGCTGGGTTTGTAGTTGACAGTTCT	10911
QY	781	GCTATTTCTTAATCAGTGGCTTGGAATCTGACAGTACCTGTTGGATTCAGCAG	840
DB	10912	GCTATTTCTTAATCAGTGGCTTGGAATCTGACAGTACCTGTTGGATTCAGCAG	10971
QY	841	GCTTATCATGATGTGCACTACTTCAACACCGTAACTGAGCTCAAGCTCACTTACT	900
DB	10972	GCTTATCATGATGTGCACTACTTCAACACCGTAACTGAGCTCAAGCTCACTTACT	11031
QY	901	CGTCTTGACTCACTGCTTACAAATCTGAATCACTTCCCAATGCTGATGCCCTTGAC	960
DB	11032	CGTCTTGACTCACTGCTTACAAATCTGAATCACTTCCCAATGCTGATGCCCTTGAC	11091
QY	961	GAACTTCGCAATGACAAACAGCGCGCTCTTCTGCTGTACCTCCGACAGAACTGCG	1020
DB	11092	GAACTTCGCAATGACAAACAGCGCGCTCTTCTGCTGTACCTCCGACAGAACTGCG	11151
QY	1021	GTCGTATGACCTCTACAGAGTAAGAACAGACAGCGGCTGTTTACAGGCAAGAGAA	1080
DB	11152	GTCGTATGACCTCTACAGAGTAAGAACAGACAGCGGCTGTTTACAGGCAAGAGAA	11211
QY	1081	CTCCAGAGAGCTGCTGATCTGTAGGCAAGCAAGCGGCAAGCGGCTGCTCCAG	1140
DB	11212	CTCCAGAGAGCTGCTGATCTGTAGGCAAGCAAGCGGCAAGCGGCTGCTCCAG	11271
QY	1141	CGCCATGACTGGAGAGGAGTGGGCTCTTCCCAATGCAAGAGAGAGATGATAG	1200
DB	11272	CGCCATGACTGGAGAGGAGTGGGCTCTTCCCAATGCAAGAGAGAGATGATAG	11331
QY	1201	GTAGCTGTGTGTGACGCTCTCAAAAGAAATGAGCGGCTGCTGTTGTGTGCTCA	1260
DB	11332	GTAGCTGTGTGTGACGCTCTCAAAAGAAATGAGCGGCTGCTGTTGTGTGCTCA	11391
QY	1261	CTGAACCTCTCTCTATCTTGCACATTCGCGGTTGTTTGTACATTAATAATG	1320
DB	11392	CTGAACCTCTCTCTATCTTGCACATTCGCGGTTGTTTGTACATTAATAATG	11451
QY	1321	CCCGTGGCTGCAAGTGAATAATCC	1344
DB	11452	CCCGTGGCTGCAAGTGAATAATCC	11475

RESULT 3  
AX756279 1119 bp DNA linear PAT 23-JUN-2003  
LOCUS Sequence 1018 from Patent WO03000905.  
DEFINITION AX756279  
ACCESSION AX756279  
VERSION AX756279.1 GI:32168410  
KEYWORDS  
SOURCE  
ORGANISM  
Triticum aestivum (bread wheat)  
Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Pooidae; Triticeae; Triticum.  
REFERENCE  
1 Zhu, T., Cheng, W., Briggs, S., Cooper, B., Goff, S.A., Moughamer, T.,  
Glazebrook, J., Katagiri, F., Kreps, J., Provart, N. and Riecke, D.  
Identification and characterization of plant genes  
Patent: WO 03000905-A 1018 03-JAN-2003;

SYNGENTA PARTICIPATIONS AG (CH)  
Location/Qualifiers  
1. .1119  
/organism="Triticum aestivum"  
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ORIGIN

Query Match 27.5%; Score 370; DB 6; Length 1119;  
Best Local Similarity 100.0%; Pred. No. 2.9e-93;  
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 961 GAACATCCGATACACACAGCCGCTCTTCTCGGATGACATCCGAGCAGAACTGCG 1020  
DB 727 GAACATCCGATACACACAGCCGCTCTTCTCGGATGACATCCGAGCAGAACTGCG 786  
QY 1021 GTGCTGTATGCTCTTACAGATTAAGACACAGCCGCTTGTTCAGAGCAGAAAGAGAA 1080  
DB 787 GTGCTGTATGCTCTTACAGATTAAGACACAGCCGCTTGTTCAGAGCAGAAAGAGAA 846  
QY 1081 CTCACAGAGCTCGTGATGTGAGCAGAGCGGCGGCGGCGGCGGCTGCTCCAG 1140  
DB 847 CTCACAGAGCTCGTGATGTGAGCAGAGCGGCGGCGGCGGCGGCTGCTCCAG 906  
QY 1141 CGGCATGACCTGGAGGGGATGCTGCTCTTCCAGATGCGAGAGAGAGATGATAG 1200  
DB 907 CGGCATGACCTGGAGGGGATGCTGCTCTTCCAGATGCGAGAGAGAGATGATAG 966  
QY 1201 GTAGCTTGTGATGAGCGCTCGAAGAAATGACGCGGCTGGGTGTTGTGCTGCA 1260  
DB 967 GTAGCTTGTGATGAGCGCTCGAAGAAATGACGCGGCTGGGTGTTGTGCTGCA 1026  
QY 1261 CTGAACCTCTCTCTCTATCTTGCATATCCCGGCTGTTTGTATCAATAAATAATG 1320  
DB 1027 CTGAACCTCTCTCTCTATCTTGCATATCCCGGCTGTTTGTATCAATAAATAATG 1086  
QY 1321 CCGGTGGCT 1330  
DB 1087 CCGGTGGCT 1096

RESULT 4  
AR340173 2853 bp DNA linear PAT 17-AUG-2003  
LOCUS AR340173  
DEFINITION Sequence 3 from patent US 6570066.  
ACCESSION AR340173  
VERSION AR340173.1 GI:33731570  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2853)  
AUTHORS Willmetts, L., Krieger, C., Lueticke, S. and Lorz, H.  
TITLE Nucleotide sequences encoding enzymes that alter the carbohydrate concentration and composition in plants  
JOURNAL Patent: US 6570066-A 3 27-MAY-2003;  
FEATURES  
Location/Qualifiers  
1. .2853  
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ORIGIN

Query Match 27.5%; Score 370; DB 6; Length 2853;  
Best Local Similarity 100.0%; Pred. No. 3.3e-93;  
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 961 GAACATCCGATACACACAGCCGCTCTTCTCGGATGACATCCGAGCAGAACTGCG 1020  
DB 727 GAACATCCGATACACACAGCCGCTCTTCTCGGATGACATCCGAGCAGAACTGCG 786  
QY 1021 GTGCTGTATGCTCTTACAGATTAAGACACAGCCGCTTGTTCAGAGCAGAAAGAGAA 1080  
DB 787 GTGCTGTATGCTCTTACAGATTAAGACACAGCCGCTTGTTCAGAGCAGAAAGAGAA 846  
QY 1081 CTCACAGAGCTCGTGATGTGAGCAGAGCGGCGGCGGCGGCGGCTGCTCCAG 1140  
DB 847 CTCACAGAGCTCGTGATGTGAGCAGAGCGGCGGCGGCGGCGGCTGCTCCAG 906  
QY 1141 CGGCATGACCTGGAGGGGATGCTGCTCTTCCAGATGCGAGAGAGAGATGATAG 1200  
DB 907 CGGCATGACCTGGAGGGGATGCTGCTCTTCCAGATGCGAGAGAGAGATGATAG 966  
QY 1201 GTAGCTTGTGATGAGCGCTCGAAGAAATGACGCGGCTGGGTGTTGTGCTGCA 1260  
DB 967 GTAGCTTGTGATGAGCGCTCGAAGAAATGACGCGGCTGGGTGTTGTGCTGCA 1026  
QY 1261 CTGAACCTCTCTCTCTATCTTGCATATCCCGGCTGTTTGTATCAATAAATAATG 1320  
DB 1027 CTGAACCTCTCTCTCTATCTTGCATATCCCGGCTGTTTGTATCAATAAATAATG 1086  
QY 1321 CCGGTGGCT 1330  
DB 1087 CCGGTGGCT 1096

CTCCAGAGAGCTCGTGATGTCGACGAAACGACGCGGCAACGCGCGGAGCTGCTCCAG 1140  
DB 2539 CTCCAGAGAGCTCGTGATGTCGACGAAACGACGCGGCAACGCGCGGAGCTGCTCCAG 2598  
QY 1141 CGGCATGACCTGGAGGGGATGCTGCTCTTCCAGATGCGAGAGAGAGATGATAG 1200  
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QY 1201 GTAGCTTGTGATGAGCGCTCGAAGAAATGACGCGGCTGGGTGTTGTGCTGCA 1260  
DB 2659 GTAGCTTGTGATGAGCGCTCGAAGAAATGACGCGGCTGGGTGTTGTGCTGCA 2718  
QY 1261 CTGAACCTCTCTCTCTATCTTGCATATCCCGGCTGTTTGTATCAATAAATAATG 1320  
DB 2719 CTGAACCTCTCTCTCTATCTTGCATATCCCGGCTGTTTGTATCAATAAATAATG 2778  
QY 1321 CCGGTGGCT 1330  
DB 2779 CCGGTGGCT 2788

RESULT 5  
TAU66376 2853 bp mRNA linear PLN 18-OCT-1996  
LOCUS TAU66376  
DEFINITION Triticum aestivum 1,4-alpha-D-glucan  
6-alpha-D-(1,4-alpha-D-glucanotransferase mRNA, complete cds.  
U66376  
U66376.1 GI:1620661  
ACCESSION U66376  
VERSION U66376  
KEYWORDS  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Triticum.  
1 (bases 1 to 2853)  
AUTHORS Krieger, C., Lorz, H. and Lueticke, S.  
TITLE Direct Submission  
JOURNAL Submitted (08-AUG-1996) University of Hamburg, Institute of General Botany, Centre of Applied Molecular Biology, AMP II, Ohnhorststr. 18, Hamburg 22609, Germany  
Location/Qualifiers  
1. .2853  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
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313. .2502  
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PQYRLMAVADKWEILIKOSDESKMGDIYHLLTNKMLIEKCVYASDSHDALVAGK  
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WIDFPRGPOTLFTGKYLPGNNNTYDKRRRFIDGDAFLIRPGMGEFDOAMCHLEKY  
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ORIGIN

Query Match 27.5%; Score 370; DB 8; Length 2853;  
Best Local Similarity 100.0%; Pred. No. 3.3e-93;





PUBMED 11244112  
2 (bases 1 to 2726)  
REFERENCE Rahman,S., Regina,A., Li,Z., Abrahams,S. and Morell,M.K.  
AUTHORS  
TITLE Direct Submission  
JOURNAL Submitted (18-JAN-2001) Plant Industry, CSIRO, Clunies Ross,  
Canberra, ACT 2601, Australia  
FEATURES  
source Location/Qualifiers  
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124..2430  
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## CDS

Query Match 26.8%; Score 360.6; DB 8; Length 2726;  
Best Local Similarity 98.4%; Pred. No. 1.5e-90;  
Matches 375; Conservative 0; Mismatches 4; Indels 2; Gaps 1;  
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1321 CCCGTGGCTCAACGTGAAA 1341  
2705 CCCGTGGCTCAACGTGAAA 2725

## ORIGIN

RESULT 8  
TASBA2 2970 bp mRNA linear PLN 27-FEB-1997  
LOCUS T.aestivum mRNA for starch branching enzyme II.  
ACCESSION Y11282  
VERSION Y11282.1 GI:1885343  
KEYWORDS 1,4-alpha-glucan branching enzyme; sbe2 gene; starch branching

SOURCE  
ORGANISM Triticum aestivum (bread wheat)  
Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Pooidae; Triticeae; Triticum.  
REFERENCE  
AUTHORS Nair,R.B., Baga,M., Scoles,G.J., Karcha,K.K. and Chibbar,R.N.  
TITLE Isolation, characterization and expression analysis of a starch  
branching enzyme II cDNA from wheat  
JOURNAL Plant Sci.  
2 (bases 1 to 2970)  
AUTHORS Chibbar,R.N.  
TITLE Direct Submission  
JOURNAL Submitted (14-FEB-1997) R.N. Chibbar, Plant Biotechnology  
Institute, National Research Council of Canada, 110 Gymnasium  
Place, Saskatoon, Saskatchewan S7N 0W9, CANADA  
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gene  
CDS

Query Match 26.8%; Score 360; DB 8; Length 2970;  
Best Local Similarity 98.2%; Pred. No. 2.2e-90;  
Matches 375; Conservative 0; Mismatches 5; Indels 2; Gaps 1;  
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2527 CGGCATGACTGAGAGGAGATGCTGCTCTTCCCAATGCCAGAGGAGAGCAGATGATAG 2586  
1201 GTAGCTTTGTTGTAGCGCTCGAAAAGAAATGACGCGGCTGGTGTGTTGTGCTGCA 1260  
2587 GTAGCTTTGTTGTAGCGCTCGAAAAGAAATGACGCGGCTGGTGTGTTGTGCTGCA 2646  
1261 CTGAACCTCTCTCTAATCTTGACATCCGCGGTGTTTTGTATATATACTAATAATTG 1320  
2647 CT-AACCTCTCTCTAATCTTGACATCCGCGGTGTTTTGTATATATACTAATAATTG 2704  
1321 CCCGTGGCTCAACGTGAAA 1341  
2705 CCCGTGGCTCAACGTGAAA 2725

## ORIGIN

RESULT 8  
TASBA2 2970 bp mRNA linear PLN 27-FEB-1997  
LOCUS T.aestivum mRNA for starch branching enzyme II.  
ACCESSION Y11282  
VERSION Y11282.1 GI:1885343  
KEYWORDS 1,4-alpha-glucan branching enzyme; sbe2 gene; starch branching

QY 1021 GTCTGTATGACCTTACAGAGTAAGAACAGACGCGCTTGTATCAAGGCAAGAGAGAA 1080  
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 QY 1141 CGCCATGATGAG 1200  
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 QY 1201 GTAGCTTGTGATGAG 1260  
 DB 2779 GTAGCTTGTGATGAG 2838  
 QY 1261 CTGAACCT 1320  
 DB 2839 CT--ACCT 2896  
 QY 1321 CCGGTGCGCTCAACGTGAAT 1342  
 DB 2897 CCGGTGCGCTCAACGTGAAT 2918

RESULT 9  
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 LOCUS AF064560  
 DEFINITION Hordeum vulgare cultivar Bomt starch branching enzyme Iia (sbeIIa)  
 mRNA, nuclear gene encoding plastid protein, complete cds.  
 ACCESSION AF064560  
 VERSION AF064560.1 GI:3822019  
 KEYWORDS  
 SOURCE Hordeum vulgare subsp. vulgare  
 ORGANISM Hordeum vulgare subsp. vulgare  
 Bacteria; Viridiplantae; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Pooidae; Triticeae; Hordeum.  
 1 (bases 1 to 2554)  
 Sun, C., Sachish, P., Ahlandsberg, S. and Jansson, C.  
 The two genes encoding starch-branching enzymes Iia and Iib are  
 differentially expressed in barley  
 Plant Physiol. 118 (1), 37-49 (1998)  
 JOURNAL 98404232  
 PUBMED 973524  
 MEDLINE 2 (bases 1 to 2554)  
 JOURNAL Sun, C., Sachish, P., Ahlandsberg, S. and Jansson, C.  
 Direct Submission  
 Submitted (11-MAY-1998) Stockholm University, Biochemistry,  
 Stockholm S-10691, Sweden  
 JOURNAL Location/Qualifiers  
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ORIGIN  
 Query Match 19.6%; Score 263.6; DB 8; Length 2554;  
 Best Local Similarity 87.5%; Pred. No. 4; Se-63;  
 Matches 343; Conservative 0; Mismatches 24; Indels 25; Gaps 4;  
 QY 961 GAACATCCGATGACACACAGGCGCGCTCTTCTGCTGTACACTCCGACGAACTGCG 1020  
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 DB 2368 GTAGCTTGTGATGAG 2427  
 QY 1244 GTG---TTGT 1299  
 DB 2428 GTGACATTTTGT 2484  
 QY 1300 TGTACATAT-ACTAATATATTGCCCGGTGCT 1330  
 DB 2485 TGTACAT 2516

RESULT 10  
 BT008928 2549 bp mRNA linear PLN 20-JUN-2003  
 LOCUS BT008928  
 DEFINITION Triticum aestivum clone wdel.f.pk002.g8.fis, full insert mRNA  
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 ACCESSION BT008928  
 VERSION BT008928.1 GI:32128479  
 KEYWORDS FLI CDNA.  
 SOURCE Triticum aestivum (bread wheat)  
 ORGANISM Triticum aestivum  
 Bacteria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Pooidae; Triticeae; Triticum.  
 1 (bases 1 to 2549)  
 Tingey, S.V., Wolterre, P., Powell, W., Dolan, M., Miao, G.-H.,  
 Caraher, N.R., Hanafey, M.K. and Hanley, C.F.  
 Direct Submission  
 Submitted (20-JUN-2003) Crop Genetics, E. I. DuPont de Nemours and  
 Company, 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104,  
 USA  
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 Best Local Similarity 90.9%; Pred. No. 2; Se-33;  
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DB 2258 CTTGCAAGAGAGAGATTTGGTATTTGTTTCAACTTCCACTGAGCAATAGCTTTTGA 2317  
QY 383 CTAACCTGTTGGTGTTCACAGCCTGGAGATGACATGCTGCTTTTCACTTGTCC 442  
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QY 443 ACCCTT 448  
DB 2378 ACTCTT 2383  
RESULT 11 1292 bp DNA linear PLN 20-APR-2003  
AY235404  
LOCUS Zea mays subsp. mays cultivar CML333 amylose extender starch-branching enzyme (ael) gene, exons 19 through 22 and partial cds.  
DEFINITION  
ACCESSION AY235404.1 GI:30026552  
VERSION  
KEYWORDS Zea mays subsp. mays (maize)  
SOURCE  
ORGANISM Zea mays subsp. mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 1292)  
AUTHORS Whitc,S.R., Wilson,L.M., Tenailon,M.I., Gaut,B.S. and Buckler,E.S.  
TITLE Genetic diversity and selection in the maize starch pathway  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)  
MEDLINE 22247734  
PUBMED 12244216  
REFERENCE 2 (bases 1 to 1292)  
AUTHORS Whitc,S.R., Wilson,L.M., Tenailon,M.I., Gaut,B.S. and Buckler,E.S.  
TITLE Direct Submision  
JOURNAL Submitted (12-FEB-2003) Genetics, USDA-ARS, North Carolina State University, 3513 Gardner Hall, Box 7614, Raleigh, NC 27695, USA  
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QY 313 AGTGATCATCTCCAAAGAGAGATTTGATTTGTTTCAACTTCCACTGAGCAATA 372  
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DB 520 TT 521  
RESULT 12 1373 bp DNA linear PLN 20-APR-2003  
AY235395  
LOCUS Zea mays subsp. mays cultivar A6 amylose extender starch-branching enzyme (ael) gene, exons 19 through 22 and partial cds.  
DEFINITION  
ACCESSION AY235395  
VERSION  
KEYWORDS Zea mays subsp. mays (maize)  
SOURCE  
ORGANISM Zea mays subsp. mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 1373)  
AUTHORS Whitc,S.R., Wilson,L.M., Tenailon,M.I., Gaut,B.S. and Buckler,E.S.  
TITLE Genetic diversity and selection in the maize starch pathway  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)  
MEDLINE 22247734  
PUBMED 12244216  
REFERENCE 2 (bases 1 to 1373)  
AUTHORS Whitc,S.R., Wilson,L.M., Tenailon,M.I., Gaut,B.S. and Buckler,E.S.  
TITLE Direct Submision  
JOURNAL Submitted (12-FEB-2003) Genetics, USDA-ARS, North Carolina State University, 3513 Gardner Hall, Box 7614, Raleigh, NC 27695, USA  
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ORIGIN

Query Match 9.9%; Score 132.4; DB 8; Length 1382;  
 Best Local Similarity 83.0%; Pred. No. 6.3e-26;  
 Matches 151; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 253 TGTAACTGCACTTATGACATCTGACACCGATGTTGTTTCACTTCAGTGAAGATA 312  
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QY 313 AGGTGATCACTCCGAAAGAGAGATTTGTTTCACTTCAGTGAAGATA 372  
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QY 373 GCTTTTGACTACCGTGTGGTGTTCAGACCTGGAGATACAGGTATGCTT 432  
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QY 433 TT 434  
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 Db 571 TT 572

RESULT 15  
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 LOCUS Zea mays subsp. mays cultivar B103 amylose extender  
 DEFINITION starch-branching enzyme (ael) gene, exons 19 through 22 and partial  
 cds.  
 AY235396  
 AY235396.1 GI:30026536

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

Zea mays subsp. mays (maize)  
 Zea mays subsp. mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 1393)  
 White, S.R., Wilson, L.M., Tenailon, M.I., Gaut, B.S. and Buckler, E.S.  
 Genetic diversity and selection in the maize starch pathway  
 Proc. Natl. Acad. Sci. U.S.A. 99 (20), 12959-12962 (2002)

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 2 (bases 1 to 1393)  
 White, S.R., Wilson, L.M., Tenailon, M.I., Gaut, B.S. and Buckler, E.S.  
 IV.  
 Direct Submission  
 Submitted (12-FEB-2003) Genetics, USDA-ARS, North Carolina State

FEATURES  
 source University, 3513 Gardner Hall, Box 7614, Raleigh, NC 27695, USA  
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 /translation="GDADYLRYHGMQEPDQMOHLEQKYEPMFSDHOYISRKHEEDKY  
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 /number=22  
 /number=22

exon  
 exon  
 exon  
 exon

ORIGIN

Query Match 9.9%; Score 132.4; DB 8; Length 1393;  
 Best Local Similarity 83.0%; Pred. No. 6.3e-26;  
 Matches 151; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 253 TGTAACTGCACTTATGACATCTGACACCGATGTTGTTTCACTTCAGTGAAGATA 312  
 |||||  
 Db 390 TGTAACTGCACTTATGACATCTGACACCGATGTTGTTTCACTTCAGTGAAGATA 449

QY 313 AGGTGATCACTCCGAAAGAGAGATTTGTTTCACTTCAGTGAAGATA 372  
 |||||  
 Db 450 AGGTGATTTGTTGAAAGAGAGATTTGTTTCACTTCAGTGAAGATA 509

QY 373 GCTTTTGACTACCGTGTGGTGTTCAGACCTGGAGATACAGGTATGCTT 432  
 |||||  
 Db 510 GCTATTTGACTACCGTATTTGTTGAAAGCTGGGGGTATAGGTATGCTATTC 569

QY 433 TT 434  
 ||  
 Db 570 TT 571

Search completed: April 10, 2004, 10:02:30  
 Job time : 5271.64 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 10, 2004, 01:51:55 ; Search time 525.86 Seconds  
(without Alignment)  
10857.595 Million cell updates/sec

Title: US-09-508-377-10\_COPY\_10120\_11463  
Perfect score: 1344  
Sequence: 1 ttatgatactgtgctatgcga.....tgcgcctcaacgtgaataacc 1344

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues  
Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_29Jan04.\*  
1: geneseqn1980s.\*  
2: geneseqn1990s.\*  
3: geneseqn2000s.\*  
4: geneseqn2001as.\*  
5: geneseqn2001bs.\*  
6: geneseqn2002s.\*  
7: geneseqn2003as.\*  
8: geneseqn2003bs.\*  
9: geneseqn2003cs.\*  
10: geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1344	100.0	11473	2 AAX34650	AAX34650 Starch br
2	1344	100.0	11475	2 AAX78338	AAX78338 Nucleotid
3	370	27.5	1119	9 ADC08713	ADC08713 Wheat DNA
4	367.4	27.3	979	3 AAZ29942	AAZ29942 Nucleotid
5	360.6	26.8	2726	3 AAX78337	AAX78337 Nucleotid
6	360	26.8	984	3 AAZ29946	AAZ29946 Nucleotid
7	347.6	25.9	977	3 AAZ29947	AAZ29947 Nucleotid
8	146	10.9	1085	3 AAZ29962	AAZ29962 Consensus
9	132.4	9.9	23449	3 AAZ25393	AAZ25393 Maize amy
10	125.6	9.3	2307	3 AAZ29938	AAZ29938 DNA encod
11	124.4	9.3	2307	3 ADC07807	ADC07807 Rice DNA
12	124.2	9.2	1120	3 AAZ29941	AAZ29941 Nucleotid
13	124	9.2	1087	3 AAZ29940	AAZ29940 Nucleotid
14	123.4	9.2	2304	9 ADC08218	ADC08218 Rice DNA
15	123.4	9.2	2555	7 ADA71289	ADA71289 Rice gene
16	123.4	9.2	3015	2 AAV05639	AAV05639 Rice type
17	122.6	9.1	1036	3 AAZ29939	AAZ29939 Nucleotid
18	122.6	9.1	2968	3 AAX78342	AAX78342 Nucleotid
19	122.4	9.1	3039	6 AAX78344	AAX78344 Nucleotid
20	122.4	9.1	1267	9 ADC08721	ADC08721 Wheat sta
21	120.6	9.0	636	9 ADC08852	ADC08852 Corn DNA
22	120.6	9.0	2640	2 AAV70961	AAV70961 DNA encod
23	120.6	9.0	2665	2 AAT69729	AAT69729 Plasmid p

24	120.6	9.0	2725	2 AAV29757	AAV29757 Zea mays
25	112.4	8.4	2919	2 AAO73750	AAO73750 Rice star
26	106.2	7.9	2283	9 ADC07805	ADC07805 Rice DNA
27	97	7.2	602	6 ABQ66378	ABQ66378 Arabidops
28	97	7.2	2418	6 ABZ13067	ABZ13067 Arabidops
29	97	7.2	2418	7 ADA68438	ADA68438 Arabidops
30	95.4	7.1	2529	2 AAT42637	AAT42637 Class A s
31	95.4	7.1	2531	2 AAT17267	AAT17267 Class A s
32	92.6	6.9	2975	2 AAT42635	AAT42635 Class A s
33	91.4	6.8	1919	2 AAV38722	AAV38722 CDNA enc
34	91.4	6.8	3090	2 AAV38720	AAV38720 Full leng
35	91	6.8	1255	7 AAD51329	AAAD51329 Potato BE
36	91	6.8	2563	5 ABK50301	ABK50301 Potato CD
37	91	6.8	2576	2 AAT42636	AAT42636 Class A s
38	91	6.8	2578	2 AAT42631	AAT42631 Class A s
39	91	6.8	3074	2 AAT69587	AAT69587 Potato st
40	89.4	6.7	3231	2 AAT42632	AAT42632 Class A s
41	89.4	6.7	1069	2 AAV38721	AAV38721 CDNA enc
42	89.4	6.7	2913	2 AAV38719	AAV38719 Full leng
43	89.4	6.7	3003	2 AAT42634	AAT42634 Class A s
44	89.4	6.7	3033	2 AAT42630	AAT42630 Class A s
45	84.4	6.3	359	3 AAA67263	AAA67263 Eucalyptu

## ALIGNMENTS

RESULT 1  
ID AAX34650 standard; DNA; 11473 BP.  
XX AAX34650;  
XX 17-OCT-2003 (revised)  
DT 05-JUL-1999 (first entry)  
XX  
DE Starch branching enzyme II (SBE II) gene sequence.  
XX  
KW Starch biosynthetic pathway; cereal plant; enzyme; SBE; SSS; DBE; GBSG;  
KW starch branching enzyme; starch soluble synthase; debranching enzyme;  
KW endosperm; wheat; barley; granule-bound synthase; glutenin; starch;  
KW grain softness protein I; bacterial isoamylase; glycogen synthase;  
KW WSBE 1-D4 gene; ss.  
XX  
OS Aegilops tauschii.  
XX  
PN WO9914314-A1.  
XX  
PD 25-MAR-1999.  
XX  
XX 11-SEP-1998; 98WO-AU000743.  
XX  
XX 12-SEP-1997; 97AU-00009108.  
PR 20-MAR-1998; 98AU-00002509.  
XX  
PA (CSTR) COMMONWEALTH SCI & IND RES ORG.  
PA (AUSU) UNIV AUSTRALIAN NAT.  
PA (GOOD-) GOODMAN FIELDER LTD.  
PA (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.  
XX  
PI Li Z, Morell M, Rahman S;  
XX  
XX WPI; 1999-229525/19.  
XX  
XX New isolated cereal plant enzyme genes used for, e.g. expression of  
PT antisense sequences of granule bound synthase.  
XX  
XX Claim 8; Page 75-81; 171pp; English.  
XX  
XX The invention relates to a novel enzyme of starch biosynthetic pathway in  
CC a cereal plant, where the enzyme is selected from starch branching enzyme  
CC (SBE) I, SBE II, starch soluble synthase (SSS) I, and debranching enzyme  
CC (DBE), with the proviso that the enzyme is not SSS I of rice, or SBE I of

CC rice or maize. The methods and products can be used for targeting  
 CC expression specifically to the endosperm of the seeds of cereal plants  
 CC such as wheat or barley. They can be used for the expression of e.g.  
 CC antisense sequences of granule-bound synthase (GBS), SBE II, low mol.  
 CC wt. glutenin, grain softness protein 1, bacterial isomylase, bacterial  
 CC glycogen synthase, and wheat high mol. wt. glutenin Bx17. They can be  
 CC used for modifying the characteristics of starch produced by a plant. The  
 CC present sequence represents the SBE II gene sequence. (Updated on 17-Oct-  
 CC 2003 to standardise OS field)  
 CC XX  
 SQ Sequence 11473 BP; 3096 A; 2263 C; 2423 G; 3691 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 1344; DB 2; Length 11473;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGATATGCTGTGATGCAAGAGTTCGATCAGGCAATGCAATCTTGAAGAAATATG 60  
 DB 10130 TTAGATATGCTGTGATGCAAGAGTTCGATCAGGCAATGCAATCTTGAAGAAATATG 10189  
 QY 61 GGGATATGCTGTGATGCTTCTTGTTCATTAACAAGTCAAGTTAAGCTCTCTTC 120  
 DB 10190 GGGATATGCTGTGATGCTTCTTGTTCATTAACAAGTCAAGTTAAGCTCTCTTC 10249  
 QY 121 AAGTGTATTAAGAGTGTATTAATTCCTGTATGATGAAACTGTGCAAGGCGG 180  
 DB 10250 AAGTGTATTAAGAGTGTATTAATTCCTGTATGATGAAACTGTGCAAGGCGG 10309  
 QY 181 AGCTGGAATGCTTTTCAACCAAACTATTTCTTAAGTCTGTGATGATACATATAC 240  
 DB 10310 AGCTGGAATGCTTTTCAACCAAACTATTTCTTAAGTCTGTGATGATACATATAC 10369  
 QY 241 CAGCACTGACATGTACTGACAGTTTATGACATCTGACACCAAGTATGTTTCAACGGAAC 300  
 DB 10370 CAGCACTGACATGTACTGACAGTTTATGACATCTGACACCAAGTATGTTTCAACGGAAC 10429  
 QY 301 ATGAGGAAGATTAAGTATCATCTCCAAAGAGAGATTTGGTATTTGTTTCAACTCC 360  
 DB 10430 ATGAGGAAGATTAAGTATCATCTCCAAAGAGAGATTTGGTATTTGTTTCAACTCC 10489  
 QY 361 ACTGAGGCAATATGCTTTTCTTGAACCTGACCTGAGGAGTCAAGCTGAGGAATACAG 420  
 DB 10490 ACTGAGGCAATATGCTTTTCTTGAACCTGACCTGAGGAGTCAAGCTGAGGAATACAG 10549  
 QY 421 TATGCTGCTTTTCAATGCTCCACCTTCAACCAAGTATGAGGTTAGTGAGGCTTCTACACT 480  
 DB 10550 TATGCTGCTTTTCAATGCTCCACCTTCAACCAAGTATGAGGTTAGTGAGGCTTCTACACT 10609  
 QY 481 TTTAATTCACATGATAGAGTTTGTGTGCTGACGCTATCAATATAAGAAATAGGGTA 540  
 DB 10610 TTTAATTCACATGATAGAGTTTGTGTGCTGACGCTATCAATATAAGAAATAGGGTA 10669  
 QY 541 ATTGTAAAGAAAGAAATTTGCTGAGCTGTGAGCCATAGGAAGTGTCTTAAACAG 600  
 DB 10670 ATTGTAAAGAAAGAAATTTGCTGAGCTGTGAGCCATAGGAAGTGTCTTAAACAG 10729  
 QY 601 CCCCAGAACACATACCATTCATTCATATATATCTAATTAAGTGTGTTTCAATCTTATG 660  
 DB 10730 CCCCAGAACACATACCATTCATTCATATATATCTAATTAAGTGTGTTTCAATCTTATG 10789  
 QY 661 CTGAGTGGACCTGGTCTTAATCTGAATATTTTCCGAATCTACCTTAACCATCTTACG 720  
 DB 10790 CTGAGTGGACCTGGTCTTAATCTGAATATTTTCCGAATCTACCTTAACCATCTTACG 10849  
 QY 721 AGTTTAAAGACAGCCCATTTTGAACATTTGCTGGGTTTGTGTTAGTTTGAAGTTTCT 780  
 DB 10850 AGTTTAAAGACAGCCCATTTTGAACATTTGCTGGGTTTGTGTTAGTTTGAAGTTTCT 10909  
 QY 781 GCTATTTCTTAATCAGTGGCTTGTGACTCTGACATGACATCTTTGTTGATTCACAG 840  
 DB 10910 GCTATTTCTTAATCAGTGGCTTGTGACTCTGACATGACATCTTTGTTGATTCACAG 10969  
 QY 841 GCTTATATATATGCTGACTTCTCAACCGTATGCTGAGGCTCAAGGCTGACTGACT 900

DB 10970 GCTTATATATATGCTGACTTCTCAACCGTATGCTGAGGCTCAAGGCTGACT 11029  
 QY 901 CGTCTTGAACCACTGCTTCAAAATCTGAATCAACTTCCATTTGCTGATCCCTTGAG 960  
 DB 11030 CGTCTTGAACCACTGCTTCAAAATCTGAATCAACTTCCATTTGCTGATCCCTTGAG 11089  
 QY 961 GAACATCCGATGACACACAGCCGCTCTTTCTCGGTGATCACTCCGAGCAAACTCG 1020  
 DB 11090 GAACATCCGATGACACACAGCCGCTCTTTCTCGGTGATCACTCCGAGCAAACTCG 11149  
 QY 1021 GTGCTGATGCTCTTCAAGATTAAGAACACAGCCGCTTGTTCACAGCAAGAGAGAA 1080  
 DB 11150 GTGCTGATGCTCTTCAAGATTAAGAACACAGCCGCTTGTTCACAGCAAGAGAGAA 11209  
 QY 1081 CTCAGAGACCTGCTGATGCTGAGCGAGACGAGCGCAACGAGGCTGCTCCAG 1140  
 DB 11210 CTCAGAGACCTGCTGATGCTGAGCGAGACGAGCGCAACGAGGCTGCTCCAG 11269  
 QY 1141 CGCATGACTGGAGAGGAGATCGTCTCTTCCAGATGCTCAGAGAGAGCATGATAG 1200  
 DB 11270 CGCATGACTGGAGAGGAGATCGTCTCTTCCAGATGCTCAGAGAGAGCATGATAG 11329  
 QY 1201 GTAGCTTGTGTTGAGAGGCTCGAAGAAATGAGCGGAGCTGGGTTGTTGTTGCTCA 1260  
 DB 11330 GTAGCTTGTGTTGAGAGGCTCGAAGAAATGAGCGGAGCTGGGTTGTTGTTGCTCA 11389  
 QY 1261 CTGAACCTCTCTCTATCTTGAACATTCGCGTGTGTTTGTATCATATATATATG 1320  
 DB 11390 CTGAACCTCTCTCTATCTTGAACATTCGCGTGTGTTTGTATCATATATATATG 11449  
 QY 1321 CCGTGGCTCTCAACGTGAATAATCC 1344  
 DB 11450 CCGTGGCTCTCAACGTGAATAATCC 11473

RESULT 2  
 AAH78338  
 ID AAH78338 standard, cDNA, 11475 BP.  
 XX  
 AC AAH78338;  
 XX  
 DT 26-NOV-2001 (first entry)  
 XX  
 DE Nucleotide sequence of a starch branching enzyme designated F2.  
 XX  
 KW Wheat; starch branching enzyme; BE1b; SBE; transgenic plant;  
 XX search biosynthetic pathway; amylopectin; F2; amylose; ss.  
 XX  
 OS Aegilops tauschii.  
 XX  
 PN WO200162834-A1.  
 XX  
 PD 30-AUG-2001.  
 XX  
 PF 21-FEB-2001, 2001MO-AU000175.  
 XX  
 PR 21-FEB-2001, 2000AU-00005742.  
 XX  
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.  
 XX (GOOD-) GOODMAN FIELDER LTD.  
 XX (LIMA-) GRP LIVAGRAIN PACIFIC PTY LTD.  
 XX  
 PI Morell M, Rahman S;  
 XX  
 DR WPI; 2001-570635/64.  
 XX  
 PT Nucleic acids encoding wheat starch branching enzyme IIb, useful for  
 XX altering the amylose and amylopectin content of cereal plants, e.g. wheat  
 XX and barley.  
 PS Example 1; Fig 2; 103pp; English.  
 XX



CC The present sequence encodes a wheat starch branching enzyme of Aegilops  
CC tauschii, designated F2. A. tauschii is likely to be the ancestral D  
CC genome donor of wheat. Probes isolated from the present sequence were  
CC used to identify type II starch branching enzymes (SBEs) in wheat,  
CC especially BE1b. The BE1b nucleic acids may be used to genetically  
CC transform cereal plants such as wheat or barley and for altering their  
CC nutritional content by modulating the starch biosynthetic pathway to vary  
CC levels of amylopectin and/or amylose produced in the plant

XX Sequence 11475 BP; 3093 A; 2259 C; 2423 G; 3689 T; 0 U; 11 Other;

Query Match 100.0%; Score 1344; DB 5; Length 11475;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGATATGCTGTATGACAGAGCTGCATGCGCAATGACAGCATCTTGAAGAAAAATATG 60  
DB TTGATATGCTGTATGACAGAGCTGCATGCGCAATGACAGCATCTTGAAGAAAAATATG 10191  
QY 61 GGGTATGCTGCTGCTTGTCTTGTGCAATACAGTCAAGTTTAACTGCTCTTC 120  
DB GGGTATGCTGCTGCTTGTCTTGTGCAATACAGTCAAGTTTAACTGCTCTTC 10251  
QY 121 AAGTGTAAAAAAGTGTGAATTAATTCCTGTATGATGAAAACTGTGCAAAAGCGG 180  
DB AAGTGTAAAAAAGTGTGAATTAATTCCTGTATGATGAAAACTGTGCAAAAGCGG 10311  
QY 181 AGCTGAATGCTTTTCCACCAAACTATTTCTTAAGTCTGTATGATACATATAC 240  
DB AGCTGAATGCTTTTCCACCAAACTATTTCTTAAGTCTGTATGATACATATAC 10312  
QY 241 CAGCATGACATGATGACAGAGTTTATGACATCTGACACCAAGTATGTTTCAAGAAC 300  
DB CAGCATGACATGATGACAGAGTTTATGACATCTGACACCAAGTATGTTTCAAGAAC 10372  
QY 301 ATGAGAGATTAAGTATGATCATCTCAAAAAGAGAGATTGTATTTTCACTTCC 360  
DB ATGAGAGATTAAGTATGATCATCTCAAAAAGAGAGATTGTATTTTCACTTCC 10432  
QY 361 ACTGAGCAATAGCTTTTGTGATACCGCTGTGGGTTCGAAAGCTGGGAAAGTACAG 420  
DB ACTGAGCAATAGCTTTTGTGATACCGCTGTGGGTTCGAAAGCTGGGAAAGTACAG 10492  
QY 421 TATGCTGCTTTTCAATGTCACCCCTTACACAGTGAAGGTTAGTGGGGCTTCTACAACT 480  
DB TATGCTGCTTTTCAATGTCACCCCTTACACAGTGAAGGTTAGTGGGGCTTCTACAACT 10552  
QY 481 TTTAATTCACATGATAGAGTTTGTGTGCTGACGCTATCATATATAAGATAGGGTA 540  
DB TTTAATTCACATGATAGAGTTTGTGTGCTGACGCTATCATATATAAGATAGGGTA 10612  
QY 541 ATTGTGAAGAAAAGATTGCTGAGCTTGTGTAGCCATAGAGAGTTGTCTTAACAG 600  
DB ATTGTGAAGAAAAGATTGCTGAGCTTGTGTAGCCATAGAGAGTTGTCTTAACAG 10672  
QY 601 CCCCAGAGACATACATTCATCATATATCTACTTAAGTGTGTTCAATCTTATG 660  
DB CCCCAGAGACATACATTCATCATATATCTACTTAAGTGTGTTCAATCTTATG 10732  
QY 661 CTCAGTTGACTGCTCTAATACATAGACATATTTCCGAATCTACCCCTAACATCTAGC 720  
DB CTCAGTTGACTGCTCTAATACATAGACATATTTCCGAATCTACCCCTAACATCTAGC 10792  
QY 721 AGTTTGAAGACACCCCATTTGACAAATTTGGCTGGGTTTGTATGTTGACGTTTCT 780  
DB AGTTTGAAGACACCCCATTTGACAAATTTGGCTGGGTTTGTATGTTGACGTTTCT 10852  
QY 781 GGTATTCTTAATCAGTGGGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 840  
DB GGTATTCTTAATCAGTGGGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 10912  
QY 841 GCTTATGATGATGAGTACTACTTCAACACCGTAAGTCTGGGCTCAAGCGCTCACTTGA 900  
DB GCTTATGATGATGAGTACTACTTCAACACCGTAAGTCTGGGCTCAAGCGCTCACTTGA 10971

DB 10972 GCTTATGATGATGAGTACTACTTCAACACCGTAAGTCTGGGCTCAAGCGCTCACTTGA 11031  
QY CGTCTTGACTCAACCTGCTTACCAATCTGATCAACTTCCCAATGCTGATGACCTTGACAG 960  
DB CGTCTTGACTCAACCTGCTTACCAATCTGATCAACTTCCCAATGCTGATGACCTTGACAG 11091  
QY 961 GAACATCCGATGACCAACAGCGCGGCTCTTCTGCTGTACACTCCGACAGAACTGCG 1020  
DB GAACATCCGATGACCAACAGCGCGGCTCTTCTGCTGTACACTCCGACAGAACTGCG 11092  
QY 1021 GTCGTGTATGCCCTTACAGAGTAAAGACAGCGGCTTGTTCAGAGCAAAAGAGAA 1080  
DB GTCGTGTATGCCCTTACAGAGTAAAGACAGCGGCTTGTTCAGAGCAAAAGAGAA 11152  
QY 1081 CTCAGAGAGCTCGTGTATGATGAGCGAAGCGAGCGGCGGAGGCTGCTCCAG 1140  
DB CTCAGAGAGCTCGTGTATGATGAGCGAAGCGAGCGGCGGAGGCTGCTCCAG 11212  
QY 1141 CGCCATGACTGGAGAGGAGTCTGCTCTTCCCAAGATCCAGAGAGAGAGATGATAG 1200  
DB CGCCATGACTGGAGAGGAGTCTGCTCTTCCCAAGATCCAGAGAGAGAGATGATAG 11272  
QY 1201 GTAGCTTGTGTGTGAGCGCTCGAAAGAAATGAGCGGCGCTGGGTGTTGTGTGCTGCA 1260  
DB GTAGCTTGTGTGTGAGCGCTCGAAAGAAATGAGCGGCGCTGGGTGTTGTGTGCTGCA 11332  
QY 1261 CTGAACCTCTCTCTATCTGACATTCGCGGTTGTTTGTATCATATACTAATAATG 1320  
DB CTGAACCTCTCTCTATCTGACATTCGCGGTTGTTTGTATCATATACTAATAATG 11392  
QY 1321 CCCGTGCGCTCAACGTAAGAAATCC 1344  
DB CCCGTGCGCTCAACGTAAGAAATCC 11452

RESULT 3  
ADCO8713  
ID ADCO8713 standard; DNA; 1119 BP.  
XX  
AC ADCO8713;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Wheat DNA sequence Seq ID1018 related to grain filling.  
XX  
XX plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;  
KW carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;  
KW tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;  
KW wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;  
KW gene; ds; plant.  
XX  
OS Triticum aestivum.  
XX  
PN WO200300905-A2.  
XX  
PD 03-JAN-2003.  
XX  
PF 21-JUN-2002; 2002WO-1B002450.  
XX  
XX 22-JUN-2001; 2001US-0300112P.  
PR 26-SEP-2001; 2001US-0325277P.  
PR 20-DEC-2001; 2001US-0342327P.  
XX  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX  
PI Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;  
PI Glaesbrook J, Katagiri F, Kreps J, Provart N, Riecke D;  
XX  
DR WPI; 2003-229341/22.  
XX  
PT New plant genes encoding polypeptides having an activity involved in or  
PT associated with the synthesis, metabolism or degradation of carbohydrates  
PT in the plant grain useful in generating plants having improved



PT nutritional properties.  
XX  
PS Disclosure; SEQ ID NO 1018; 130pp; English.  
XX  
CC This invention, in the area of plant biotechnology, relates to novel  
CC polynucleotides comprising a nucleotide sequence encoding a protein which  
CC is involved in or associated with the synthesis, metabolism or  
CC degradation of carbohydrates in the plant grain and the expression of  
CC which is up-regulated during grain filling. The plant is selected from  
CC corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,  
CC sugarbeet, wheat, and rice. The invention may be useful for the  
CC improvement of protein, oil, starch, fibre and moisture content of the  
CC cereal grains. In addition, carbohydrate levels may be modified to a more  
CC desirable level using the present invention. The present sequence is a  
CC DNA sequence from wheat which showed homology to rice "grain filling"  
CC genes of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification, but was obtained in electronic  
CC format directly from WIPO at ftp.wipo.int/pub/publishedpct\_sequences.  
SQ  
Sequence 1119 BP; 295 A; 234 C; 291 G; 299 T; 0 U; 0 Other;  
Query Match 27.5%; Score 370; DB 9; Length 1119;  
Best Local Similarity 100.0%; Pred. No. 9,4e-106; Indels 0; Gaps 0;  
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 961 GAACATCCGCATGACACAGAGCGCGCTCTTTCGCTGTAACCTCCGACGAACTGCG 1020  
DB 727 GAACATCCGCATGACACAGAGCGCGCTCTTTCGCTGTAACCTCCGACGAACTGCG 786  
OY 1021 GTCGTGTATGCCCTTACAGAGTAAGAACAGCAGCGGCTGTATCAAGCAAGAGAGAA 1080  
DB 787 GTCGTGTATGCCCTTACAGAGTAAGAACAGCAGCGGCTGTATCAAGCAAGAGAGAA 846  
OY 1081 CTCCTAAGAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140  
DB 847 CTCCTAAGAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 906  
OY 1141 CCGCATGATGAGGAGGAGATGCTGCTCTTCCCAATGACAGAGAGAGAGAGATGATGATG 1200  
DB 907 CCGCATGATGAGGAGGAGATGCTGCTCTTCCCAATGACAGAGAGAGAGAGATGATG 966  
OY 1201 GATGCTTGTGTGAGCGCTCGAAGAAATGACGCGGCTGTGTTGTGCTGCA 1260  
DB 967 GATGCTTGTGTGAGCGCTCGAAGAAATGACGCGGCTGTGTTGTGCTGCA 1026  
OY 1261 CTGAACCTCTCTCTATCTTGCACATCCCGGTTGTTTGTATATATATATATG 1320  
DB 1027 CTGAACCTCTCTCTATCTTGCACATCCCGGTTGTTTGTATATATATATG 1086  
OY 1321 CCGGTGCGCT 1330  
DB 1087 CCGGTGCGCT 1096  
RESULT 4  
AAZ99942  
ID AAZ99942 standard; DNA; 979 BP.  
XX  
AC AAZ99942;  
XX  
DT 25-JUL-2000 (first entry)  
XX  
DE Nucleotide sequence of starch branching enzyme II clone B1.  
XX  
XX wheat; starch branching enzyme II; SBRII, SBRII-2, starch; SBRII-1,  
XX gelatinisation onset; transgenic plant; foodstuff; bakery product; ss.  
XX  
OS Triticum aestivum.  
XX  
PN MO200015810-A1.  
XX  
PD 23-MAR-2000.  
XX

PF 09-SEP-1999; 99WO-GB003011.  
XX  
PR 10-SEP-1998; 99EP-00307337.  
XX  
XX (PLAN-) PLANT BREEDING INT CAMBRIDGE LTD.  
XX  
XX Goldsborough A, Collier S;  
XX  
DR WPI; 2000-271446/23.  
XX  
PT DNA encoding wheat starch branching enzyme II isoforms, useful in  
PT altering the characteristics of a plant, especially elevated starch  
PT gelatinization onset and/or peak temperature.  
XX  
PS Claim 5; Page 124; 197pp; English.  
XX  
CC The present sequence represents a clone of wheat starch branching enzyme  
CC II (SBRII), which is part of a novel subclass of known SBRII genes,  
CC designated SBRII-2, subclass B (SBRII-2B). The specification also  
CC describes subclasses SBRII-1 genes, which are thought to have similar  
CC functional properties to the maize SBRII gene. Starch branching enzymes  
CC catalyse the formation of the alpha-1,6 linkages, creating branch points  
CC in the growing starch molecule, via hydrolysis of an alpha-1,4 linkage  
CC followed by reattachment of the released alpha-1,4-glucan chain to the  
CC same or another glucosyl chain. SBRII polypeptides can be used to alter  
CC the characteristics of a plant, in particular to alter starch so that it  
CC has an elevated gelatinisation onset and/or peak temperature. Starch  
CC obtained from transgenic plants is useful in the preparation or  
CC processing a foodstuff, particularly bakery products  
XX  
SQ Sequence 979 BP; 271 A; 203 C; 247 G; 257 T; 0 U; 1 Other;  
Query Match 27.3%; Score 367.4; DB 3; Length 979;  
Best Local Similarity 99.5%; Pred. No. 5.8e-105; Indels 0; Gaps 0;  
Matches 368; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 961 GAACATCCGCATGACACAGCGCGCTCTTTCGCTGTAACCTCCGACGAACTGCG 1020  
DB 558 GAACATCCGCATGACACAGCGCGCTCTTTCGCTGTAACCTCCGACGAACTGCG 617  
OY 1021 GTCGTGTATGCCCTTACAGAGTAAGAACAGCAGCGGCTGTATCAAGCAAGAGAGAA 1080  
DB 618 GTCGTGTATGCCCTTACAGAGTAAGAACAGCAGCGGCTGTATCAAGCAAGAGAGAA 677  
OY 1081 CTCCTAAGAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140  
DB 678 CTCCTAAGAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 737  
OY 1141 CCGCATGATGAGGAGGAGATGCTGCTCTTCCCAATGACAGAGAGAGAGATGATGATG 1200  
DB 738 CCGCATGATGAGGAGGAGATGCTGCTCTTCCCAATGACAGAGAGAGAGATGATGATG 797  
OY 1201 GATGCTTGTGTGAGCGCTCGAAGAAATGACGCGGCTGTGTTGTGCTGCA 1260  
DB 798 GATGCTTGTGTGAGCGCTCGAAGAAATGACGCGGCTGTGTTGTGCTGCA 857  
OY 1261 CTGAACCTCTCTCTATCTTGCACATCCCGGTTGTTTGTATATATATATATG 1320  
DB 858 CTGAACCTCTCTCTATCTTGCACATCCCGGTTGTTTGTATATATATATG 917  
OY 1321 CCGGTGCGCT 1330  
DB 918 CCGGTGCGCT 927  
RESULT 5  
AAH78337  
ID AAH78337 standard; cDNA; 2726 BP.  
XX  
AC AAH78337;  
XX  
DT 26-NOV-2001 (first entry)  
XX

DE Nucleotide sequence of wheat starch branching enzyme 9 (BEIIa).  
XX Wheat; starch branching enzyme; BEIIa; BEIIb; SBE; transgenic plant;  
KW starch biosynthetic pathway; amylopectin; amylose; ss.  
XX  
OS Triticum sp.  
XX WO200162934-A1.  
XX  
XX 30-AUG-2001.  
XX  
XX 21-FEB-2001; 2001WO-AU000175.  
XX  
XX 21-FEB-2000; 2000AU-00005742.  
XX  
XX (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
XX (GOOD-) GOODMAN FIELDER LTD.  
XX (LIMA-) GRP LIMAGRAIN PACIFIC PTY LTD.  
XX  
XX Morell M, Rahman S;  
XX PI  
XX WPI; 2001-570635/64.  
XX  
XX Nucleic acids encoding wheat starch branching enzyme IIb, useful for  
XX altering the amylose and amylopectin content of cereal plants, e.g. wheat  
XX and barley.  
XX  
XX Example 1; Fig 1; 103pb; English.  
XX  
XX The present sequence encodes wheat starch branching enzyme 9, designated  
XX BEIIa. The specification describes BEIIb. BEIIb is a type II starch  
XX branching enzyme (SBE). The BEIIb nucleic acids may be used to  
XX genetically transform cereal plants such as wheat or barley and for  
XX altering their nutritional content by modulating the starch biosynthetic  
XX pathway to vary levels of amylopectin and/or amylose produced in the  
XX plant  
XX  
XX Sequence 2726 BP; 726 A; 564 C; 701 G; 735 T; 0 U; 0 Other;  
SQ  
Query Match 26.8%; Score 360.6; DB 5; Length 2726;  
Best Local Similarity 98.4%; Pred. No. 1.5e-102;  
Matches 375; Conservative 0; Mismatches 4; Indels 2; Gaps 1;  
OY 961 GAACATCCGCATGACAAACAGCGCGCTCTTTCTCGGTACACTCCGAGCAAACTGCG 1020  
DB 2347 GAACATCCGCATGACAAACAGCGCGCTCTTTCTCGGTACACTCCGAGCAAACTGCG 2406  
OY 1021 GTCGTGTATGCCCTTACAGAGTAAGAAACAGCGCGCTGTTTACAGAGCAAGAGAA 1080  
DB 2407 GTCGTGTATGCCCTTACAGAGTAAGAAACAGCGCGCTGTTTACAGAGCAAGAGAA 2466  
OY 1081 CTCGAGAGAGCTCGTGATCGTAGCGAAGCGAAGCGGCGAAGCGGCGGCTGCTCCAG 1140  
DB 2467 CTCGAGAGAGCTCGTGATCGTAGCGAAGCGAAGCGGCGAAGCGGCGGCTGCTCCAG 2526  
OY 1141 CGCCATGACTGGAGAGGAGATCGTGCTCTTCCCAAGATGCCAGAGAGAGAGATGATAG 1200  
DB 2527 CGCCATGACTGGAGAGGAGATCGTGCTCTTCCCAAGATGCCAGAGAGAGAGATGATAG 2586  
OY 1201 GTAGCTGTGTGGAGAGCGCTCGAAGAAATGAGCGGCGCTGGGTGTTGTGTCGCGCA 1260  
DB 2587 GTAGCTGTGTGGAGAGCGCTCGAAGAAATGAGCGGCGCTGGGTGTTGTGTCGCGCA 2646  
OY 1261 CTGAACCTCTCTCTCTATCTGTGACATCCCGGTGTTTGTATCATATAATTAATTG 1320  
DB 2647 CT--ACCTCTCTCTATCTGTGACATCCCGGTGTTTGTATCATATAATTAATTG 2704  
OY 1321 CCGGTGCGCTCAACGTGAAA 1341  
DB 2705 CCGGTGCGCTCAACGTGAAA 2725

AA299946  
ID AA299946 standard; DNA; 984 BP.  
XX  
XX AA299946;  
XX  
XX 25-JUL-2000 (first entry)  
XX  
XX Nucleotide sequence of starch branching enzyme II clone AZ.  
XX  
XX Wheat; starch branching enzyme II; SBEII; SBEII-1; starch; SBEII-2;  
XX gelatinisation onset; transgenic plant; foodstuff; bakery product; ss.  
XX  
XX Triticum aestivum.  
XX  
XX WO200015810-A1.  
XX  
XX 23-MAR-2000.  
XX  
XX 09-SEP-1999; 99WO-GB003011.  
XX  
XX 10-SEP-1998; 98EP-00307337.  
XX  
XX (PLAN-) PLANT BREEDING INT CAMBRIDGE LTD.  
XX  
XX Goldsbrough A, Colliver S;  
XX PI  
XX WPI; 2000-271446/23.  
XX  
XX DNA encoding wheat starch branching enzyme II isoforms, useful in  
XX altering the characteristics of a plant, especially elevated starch  
XX gelatinization onset and/or peak temperature.  
XX  
XX Disclosure; Page 168; 197pb; English.  
XX  
XX The present sequence represents a clone of wheat starch branching enzyme  
XX II (SBEII), which is part of a novel subclass of known SBEII genes,  
XX designated SBEII-1. The specification also describes subclass SBEII-2  
XX sequences. The SBEII-1 genes are thought to have similar functional  
XX properties to the maize SBEIIb gene. Starch branching enzymes catalyse  
XX the formation of the alpha-1,6 linkages, creating branch points in the  
XX growing starch molecule, via hydrolysis of an alpha-1,4 linkage followed  
XX by reattachment of the released alpha-1,4-glucan chain to the same or  
XX another glucosyl chain. SBEII polypeptides can be used to alter the  
XX characteristics of a plant, in particular to alter starch so that it has  
XX an elevated gelatinisation onset and/or peak temperature. Starch obtained  
XX from transgenic plants is useful in the preparation or processing a  
XX foodstuff, particularly bakery products  
SQ  
Sequence 984 BP; 268 A; 212 C; 250 G; 254 T; 0 U; 0 Other;  
Query Match 26.8%; Score 360; DB 3; Length 984;  
Best Local Similarity 98.2%; Pred. No. 1.3e-102;  
Matches 375; Conservative 0; Mismatches 5; Indels 2; Gaps 1;  
OY 961 GAACATCCGCATGACAAACAGCGCGCTCTTTCTCGGTATACACTCCGAGCAAACTGCG 1020  
DB 558 GAACATCCGCATGACAAACAGCGCGCTCTTTCTCGGTATACACTCCGAGCAAACTGCG 617  
OY 1021 GTCGTGTATGCCCTTACAGAGTAAGAAACAGCGCGCTGTTTACAGAGCAAGAGAA 1080  
DB 618 GTCGTGTATGCCCTTACAGAGTAAGAAACAGCGCGCTGTTTACAGAGCAAGAGAA 677  
OY 1081 CTCGAGAGAGCTCGTGATCGTAGCGAAGCGAAGCGGCGAAGCGGCGGCTGCTCCAG 1140  
DB 678 CTCGAGAGAGCTCGTGATCGTAGCGAAGCGAAGCGGCGAAGCGGCGGCTGCTCCAG 737  
OY 1141 CGCCATGACTGGAGAGGAGATCGTGCTCTTCCCAAGATGCCAGAGAGAGAGATGATAG 1200  
DB 738 CGCCATGACTGGAGAGGAGATCGTGCTCTTCCCAAGATGCCAGAGAGAGAGATGATAG 797  
OY 1201 GTAGCTGTGTGGAGAGCGCTCGAAGAAATGAGCGGCGCTGGGTGTTGTGTCGCGCA 1260  
DB 798 GTAGCTGTGTGGAGAGCGCTCGAAGAAATGAGCGGCGCTGGGTGTTGTGTCGCGCA 857

QY 1261 CTGAACCTCCTCCCTATCTTGACATTCGCGTTGTTTTGTACATATACTAATAATTG 1320  
DB 858 CT-AACCTCCTCCTATCTTGACATTCGCGTTGTTTTGTACATATACTAATAATTG 915  
QY 1321 CCCGTCGCTCAACGTGAAAT 1342  
DB 916 CCGTGCCTCAACGTGAAAT 937

RESULT 7  
AAZ99947  
ID AAZ99947 standard; DNA; 977 BP.  
XX AAZ99947;  
XX  
XX 25-JUL-2000 (first entry)

DE Nucleotide sequence of starch branching enzyme II clone B11.  
XX  
XX Wheat; starch branching enzyme II; SBEII-1; starch; SBEII-2; starch; SBEII-2;  
XX gelatinisation onset; transgenic plant; foodstuff; bakery product; ss.  
XX  
XX Triticum aestivum.  
XX  
XX  
XX Key Location/Qualifiers  
XX CDS 3..641  
XX FT /\*tag= a  
XX FT /product= "starch branching enzyme II"

XX WO200015810-A1.  
XX 23-MAR-2000.  
XX  
XX 09-SEP-1999; 99WO-GB003011.  
XX  
XX 10-SEP-1998; 98EP-00307337.  
XX  
XX (PLAN-) PLANT BREEDING INT CAMBRIDGE LTD.  
XX  
XX Goldsbrough A, Colliver S;  
XX  
XX MPI; 2000-271446/23.  
XX P-PSDB; AAY84411.  
XX  
XX DNA encoding wheat starch branching enzyme II isoforms, useful in  
XX altering the characteristics of a plant, especially elevated starch  
XX gelatinization onset and/or peak temperature.  
XX  
XX  
XX Disclosure; Page 168-169; 197pp; English.  
XX  
XX The present sequence represents a clone of wheat starch branching enzyme  
XX II (SBEII), which is part of a novel subclass of known SBEII genes,  
XX designated SBEII-1. The specification also describes subclass SBEII-2  
XX sequences. The SBEII-1 genes are thought to have similar functional  
XX properties to the maize SBEIIb gene. Starch branching enzymes catalyse  
XX the formation of the alpha-1,6 linkages, creating branch points in the  
XX growing starch molecule, via hydrolysis of an alpha-1,4 linkage followed  
XX by reattachment of the released alpha-1,4-glucan chain to the same or  
XX another glucosyl chain. SBEII polypeptides can be used to alter the  
XX characteristics of a plant, in particular to alter starch so that it has  
XX an elevated gelatinisation onset and/or peak temperature. Starch obtained  
XX from transgenic plants is useful in the preparation or processing a  
XX foodstuff, particularly bakery products

XX  
XX Sequence 977 BP; 270 A; 200 C; 245 G; 262 T; 0 U; 0 Other;  
XX  
XX Query Match 25.9%; Score 347.6; DB 3; Length 977;  
XX Best Local Similarity 96.2%; Pred. No. 1.1e-98;  
XX Matches 356; Conservative 0; Mismatches 14; Indels 0; Gaps 0;  
XX  
XX 961 GAATATCCGCTGACACAGGCGCGCTTCTTGCGGTACATCCGAGCAGAACTGCG 1020

DB 558 GAATATCCGCTGACACATAGGCGCGCTTCTTGCGGTACATCTCTAGCAGAACTGCG 617  
QY 1021 GTCGTATATGCGCTTACAGAGTACAGACAGCGCGCTTGTACAGCGAAAGAGAA 1080  
DB 618 GTCGTATATGCGCTTACAGAGTACAGACAGCGCGCTTGTACAGCGAAAGAGAA 677  
QY 1081 CTCGAGAGAGCTCTGTGATTCGTGACCGAAGCGAGCGCGAGGCTGCTCCAAAG 1140  
DB 678 CTCGAGAGAGCTCTGTGATTCGTGACCGAAGCGAGCGAGGCTGCTCCAAAG 737  
QY 1141 CGCCATGACTGAGAGGAGATGCGCTCTTCCCGAGATCCAGAGAGAGATGATAG 1200  
DB 738 CGCCATGACTGAGAGGAGATGCGCTCTTCCCGAGATCCAGAGAGAGATGATAG 797  
QY 1201 GTAGCTTGTGCTGAGCGCTCGAAAGAAATGAGCGGCGCTGCTGCTGCA 1260  
DB 798 GTAGCTTGTGCTGAGCGCTCGAAAGAAATGAGCGGCGCTGCTGCTGCA 857

QY 1261 CTGAACCTCCTCCCTATCTTGACATTCGCGTTGTTTTGTACATATACTAATAATTG 1320  
DB 858 CTGAACCTCCTCCCTATCTTGACATTCGCGTTGTTTTGTACATATACTAATAATTG 917  
QY 1321 CCCGTCGCT 1330  
DB 918 CCGTGCCT 927

RESULT 8  
AAZ99962  
ID AAZ99962 standard; DNA; 1085 BP.  
XX AAZ99962;  
XX  
XX 25-JUL-2000 (first entry)

DE Consensus sequence of starch branching enzyme II.  
XX  
XX Wheat; starch branching enzyme II; SBEII; SBEII-1; starch; SBEII-2;  
XX gelatinisation onset; transgenic plant; foodstuff; bakery product; ss.  
XX  
XX Triticum aestivum.  
XX  
XX  
XX WO200015810-A1.  
XX 23-MAR-2000.  
XX  
XX 09-SEP-1999; 99WO-GB003011.  
XX  
XX 10-SEP-1998; 98EP-00307337.  
XX  
XX (PLAN-) PLANT BREEDING INT CAMBRIDGE LTD.  
XX  
XX Goldsbrough A, Colliver S;  
XX  
XX MPI; 2000-271446/23.  
XX  
XX DNA encoding wheat starch branching enzyme II isoforms, useful in  
XX altering the characteristics of a plant, especially elevated starch  
XX gelatinization onset and/or peak temperature.  
XX  
XX  
XX Disclosure; Page 187; 197pp; English.  
XX  
XX The present sequence represents the consensus sequence of wheat starch  
XX branching enzyme II (SBEII). The specification describes novel subclasses  
XX of SBEII, designated SBEII-1 and SBEII-2. The SBEII-1 genes are thought  
XX to have similar functional properties to the maize SBEIIb gene. Starch  
XX branching enzymes catalyse the formation of the alpha-1,6 linkages,  
XX creating branch points in the growing starch molecule, via hydrolysis of  
XX an alpha-1,4 linkage followed by reattachment of the released alpha-1,4-  
XX glucan chain to the same or another glucosyl chain. SBEII polypeptides  
XX can be used to alter the characteristics of a plant, in particular to  
XX alter starch so that it has an elevated gelatinisation onset and/or peak  
XX temperature. Starch obtained from transgenic plants is useful in the

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CC preparation or processing a foodstuff, particularly bakery products
XX Sequence 1085 BP; 268 A; 185 C; 284 G; 348 T; 0 U; 0 Other;
SQ
Query Match 10.9%; Score 146; DB 3; Length 1085;
Best Local Similarity 86.6%; Pred. No. 6.5e-35;
Matches 161; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 263 GTTATGACATCTGAGACCACTATGTTTACGGAACAAGAGAAATAGATGATCAT 322
    |||||
DB 326 GTTTATGACATCTGAGACCACTATGTTTCTCGAAACATAGAGAAATAGATGATCAT 385
    |||||
QY 323 CCTCAAAAGAGAGATTTGGTATTTGTTTCACTTCAGAGCAATAGCTTTTGA 382
    |||||
DB 386 GTTTGAAAGAGAGATTTGGTATTTGTTTCACTTCAGAGCAATAGCTTTTGA 445
    |||||
QY 383 CTACCGTGTGGTGTCTCCAGCGCTGGAGATACAAGATAGCTTGCTTTTCATTGTCC 442
    |||||
DB 446 CTACCGTGTGGTGTCTCCAGCGCTGGAGATACAAGATAGCTTGCTTGACCTCCAGCGCTGG 505
    |||||
QY 443 ACCCTT 448
    |||||
DB 506 ACTCTT 511
    |||||

RESULT 9
AAZ35393 ID AAZ35393 standard; DNA; 23449 BP.
XX AC AAZ35393;
XX AC 27-MAR-2000 (first entry)
DT
XX 27-MAR-2000 (first entry)
DE Maize amylose-extender (Ae) gene encoding starch branching enzyme.
XX
XX Starch branching enzyme Iib; amylose-extender gene; Ae gene; maize; corn;
KM promoter; expression control element; endosperm; transgenic plant; ss.
XX
XX Zea mays.
OS
XX
XX Key Location/Qualifiers
XX misc_signal 597..602
    /tag= a
    /note= "I box, conserved in RBGS genes"
FT repeat_unit 1475..1481
    /tag= b
    /note= "RY repeat, distal regulatory element"
FT misc_signal 1967..1973
    /tag= c
    /note= "Hex, conserved element found in plant histone
    gene promoters"
FT misc_signal 2593..2599
    /tag= d
    /note= "KRE box, motif essential for metal ion-dependent
    induction of metallothionein genes"
FT GC_signal 2666..2671
    /tag= e
    /note= "KRE box, motif essential for metal ion-dependent
    induction of metallothionein genes"
FT GC_signal 2738..2743
    /tag= f
    /note= "KRE box, motif essential for metal ion-dependent
    induction of metallothionein genes"
FT GC_signal 2831..2836
    /tag= g
    /note= "KRE box, motif essential for metal ion-dependent
    induction of metallothionein genes"
FT misc_signal 2838..2844
    /tag= h
    /note= "KRE box, motif essential for metal ion-dependent
    induction of metallothionein genes"
FT GC_signal 2874..2879
    /tag= i
    /note= "KRE box, motif essential for metal ion-dependent
    induction of metallothionein genes"
FT TATA_signal 2933..2936
    /tag= j
    /note= "KRE box, motif essential for metal ion-dependent
    induction of metallothionein genes"
FT exon 2965..3176
    /tag= k
    /note= "KRE box, motif essential for metal ion-dependent
    induction of metallothionein genes"
FT CDS 3065..119659
    /tag= l
    /note= "KRE box, motif essential for metal ion-dependent
    induction of metallothionein genes"

FT /tag= k
FT /note= "contains introns"
FT 3177..3282
    /tag= m
    /number= 1
FT exon 3283..3428
    /tag= n
    /number= 2
FT intron 3429..3672
    /tag= o
    /number= 2
FT exon 3673..3827
    /tag= p
    /number= 3
FT intron 3828..4913
    /tag= q
    /number= 3
FT exon 4914..5012
    /tag= r
    /number= 4
FT intron 5013..5088
    /tag= s
    /number= 4
FT exon 5089..5131
    /tag= t
    /number= 5
FT intron 5132..5327
    /tag= u
    /number= 5
FT exon 5328..5387
    /tag= v
    /number= 6
FT intron 5388..5886
    /tag= w
    /number= 6
FT exon 5887..5967
    /tag= x
    /number= 7
FT intron 5968..6048
    /tag= y
    /number= 7
FT exon 6049..6165
    /tag= z
    /number= 8
FT intron 6166..6750
    /tag= aa
    /number= 8
FT exon 6751..6816
    /tag= ab
    /number= 9
FT intron 6817..7591
    /tag= ac
    /number= 9
FT exon 7592..7713
    /tag= ad
    /number= 10
FT intron 7714..8464
    /tag= ae
    /number= 10
FT exon 8465..8584
    /tag= af
    /number= 11
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    /tag= ag
    /number= 11
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    /tag= ah
    /number= 12
FT intron 12735..12820
    /tag= ai
    /number= 12
FT exon 12821..12931
    /tag= aj
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FT /number= 13
FT intron 12932. .13079
FT /*tag= ak
FT /number= 13
FT exon 13080. .13208
FT /*tag= al
FT /number= 14
FT intron 13209. .16259
FT /*tag= am
FT /number= 14
FT exon 16260. .16363
FT /*tag= an
FT /number= 15
FT intron 16364. .17235
FT /*tag= ao
FT /number= 15
FT exon 17236. .17380
FT /*tag= ap
FT /number= 16
FT intron 17381. .17837
FT /*tag= aq
FT /number= 16
FT exon 17838. .17985
FT /*tag= ar
FT /number= 17
FT intron 17986. .18129
FT /*tag= as
FT /number= 17
FT exon 18130. .18230
FT /*tag= at
FT /number= 18
FT intron 18231. .18458
FT /*tag= au
FT /number= 18
FT exon 18457. .18534
FT /*tag= av
FT /number= 19
FT intron 18535. .18800
FT /*tag= aw
FT /number= 19
FT exon 18801. .18956
FT /*tag= ax
FT /number= 20
FT intron 18957. .19404
FT /*tag= ay
FT /number= 20
FT exon 19405. .19479
FT /*tag= az
FT /number= 21
FT intron 19480. .19575
FT /*tag= ba
FT /number= 21
FT exon 19576. .19659
FT /*tag= bb
FT /number= 22
FT polyA_signal 19843. .19849
FT /*tag= bc
FT misc_feature 23089. .23101
FT /*tag= bd
XX WO9964562-A2.
XX PN
XX 16-DEC-1999.
XX PD
XX 11-JUN-1999; 99WO-US013266.
XX PF
XX 12-JUN-1998; 98US-0089049P.
XX PR 12-JUN-1998; 98US-0089050P.
XX XX
XX (UYPE-) UNIV PENNSYLVANIA STATE.
XX PI
XX Guiltinan MJ, Kim K.
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DR WPI; 2000-116538/10.
XX XX
XX New gene regulatory sequences from plants used to provide resistance to
XX PT microbial path pathogens.
XX PS Claim 19; Page 98-105; 110pp; English.
XX CC This is the nucleotide sequence of the maize amylose-extender (Ae) gene

Query Match 9.9%; Score 132.4; DB 3; Length 23449;
Best Local Similarity 83.0%; Pred. No. 8.3e-30;
Matches 151; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 253 TGTAACTGCGATTATGACATCTGAGCACCAGATGATGTTTCACGAAACATGAGAGATA 312
DB 18790 TGTAACTGCGATTATGACATCTGATCACCAGATATTTCCCGAAACATGAGAGATA 18849
QY 313 AGGTGATCATCTCCAAAGAGAGATTGGTATTTTCAACTTCGACTGAGCAATA 372
DB 18850 AGGTGATGTTGTGGAAGGAGATTGGTATTTGTTCAACTTCGACTGCAACA 18909
QY 373 GCTTTTGTACTACCGTGTGGGTGTTCCAGCCTGGGAGTACAGATATGCTTGCTT 432
DB 18910 GCTATTTTACACCTGATTTGTTGTGCAAAAGCTGGGTGTATAGGTATGATCATATC 18969
QY 433 TT 434
DB 18970 TT 18971

RESULT 10
AAZ99938
ID AAZ99938 standard; DNA; 2307 BP.
XX AC
XX AAZ99938;
XX XX
XX 25-UTL-2000 (first entry)
XX DE
XX DNA encoding part of starch branching enzyme II clone 5A1.
XX KM
XX Wheat; starch branching enzyme II; SBEII; SBEII-1; starch;
XX KM gelatinisation onset; transgenic plant; foodstuff; bakery product; ss.
XX OS
XX Triticum aestivum.
XX OS
XX FH
XX Key Location/Qualifiers
FT 1. .2307
FT CDS
FT /*tag= a
FT /product= "starch branching enzyme II"
FT /transl_except= (pos: 2036. .2038, aa: Xaa)
FT /transl_except= (pos: 2051. .2053, aa: Xaa)
FT /transl_except= (pos: 2090. .2092, aa: Xaa)
FT /transl_except= (pos: 2096. .2098, aa: Xaa)
FT /transl_except= (pos: 2114. .2116, aa: Xaa)
FT /transl_except= (pos: 2147. .2149, aa: Xaa)
FT /transl_except= (pos: 2168. .2170, aa: Xaa)
FT /transl_except= (pos: 2174. .2176, aa: Xaa)
FT /transl_except= (pos: 2189. .2191, aa: Xaa)
FT /transl_except= (pos: 2267. .2269, aa: Xaa)
FT /transl_except= (pos: 2270. .2272, aa: Xaa)
FT /transl_except= (pos: 2306. .2307, aa: Xaa)
FT /note= "Xaa is an unknown amino acid; the sequence
contains 10 internal stop codons, but no termination
codon"
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(PLAN-) PLANT BREEDING INT CAMBRIDGE LTD.

PA Goldsbrough A, Colliver S;  
XX  
PI  
XX  
DR WPI: 2000-271446/23.  
XX P-PSDB: AA84408.

XX DNA encoding wheat starch branching enzyme II isoforms, useful in  
PT altering the characteristics of a plant, especially elevated starch  
PT gelatinization onset and/or peak temperature.

PS Disclosure; Fig 10; 197pp; English.

XX The present sequence encodes a wheat starch branching enzyme II (SBEII)  
CC of a novel subclass of known SBEII genes, designated SBEII-1. The SBEII-1  
CC genes are thought to have similar functional properties to the maize  
CC SBEIIb gene. Starch branching enzymes catalyse the formation of the alpha  
CC -1,6 linkages, creating branch points in the growing starch molecule, via  
CC hydrolysis of an alpha-1,4 linkage followed by reattachment of the  
CC released alpha-1,4-glucan chain to the same or another glucosyl chain.  
CC SBEII polypeptides can be used to alter the characteristics of a plant,  
CC in particular to alter starch so that it has an elevated gelatinization  
CC onset and/or peak temperature. Starch obtained from transgenic plants is  
CC useful in the preparation or processing a foodstuff, particularly bakery  
CC products

XX Sequence 2307 BP; 674 A; 440 C; 544 G; 635 T; 0 U; 14 Other;

XX Query Match 9.3%; Score 125.6; DB 3; Length 2307;  
Best Local Similarity 85.4%; Pred. No. 2.9e-28;  
Matches 140; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 264 TTTATGACATCTGAGACACAGTATGTTTCACGGAACATGAGAAAGATGATCATC 323  
DB 1508 TTTATGACATCTGAGACACAGTATGTTTCGGAACATGAGAAAGATGATCATC 1567

QY 324 CTCAAAAGAGAGATTGTTGTTTTCACCTTCACCTGAGACATAGTTTTCAC 383  
DB 1568 TTTGAAAAAGGGAGCTTGTTGTTTTCACCTTCACCTGAGATATAGCTATTTCGAC 1627

QY 384 TACCGTGTGGGTTCACAGCTCGGAGATACAAAGGTATGCTT 427  
DB 1628 TACCGGTGTGGCTGTTTAAAGCTCGGAGATACAAAGGTATGCTT 1671

RESULT 11

ADCC07807  
ID ADCC07807 standard; DNA; 2307 BP.

XX ADCC07807;

DT 18-DEC-2003 (first entry)

DE Rice DNA sequence seq ID73 related to grain filling.

XX plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;  
KW carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;  
KW tomato; banana; canola; cotton; peanut; tobacco; sugarcane;  
KW wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;  
KW gene; de; plant.

XX Oryza sativa.

XX WO2003000905-A2.

XX 03-JAN-2003.

XX 21-JUN-2002; 2002MO-IB002450.

XX 22-JUN-2001; 2001US-0300112P.

XX 26-SEP-2001; 2001US-0325277P.

XX 20-DEC-2001; 2001US-0342327P.

PA (SYGN ) SYNGENTA PARTICIPATIONS AG.

XX Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;  
PI Glazebrook J, Katagiri F, Kreps J, Provart N, Riecke D;  
XX

DR WPI: 2003-229341/22.

XX P-PSDB: ADCC07808.

XX New plant genes encoding polypeptides having an activity involved in or  
PT associated with the synthesis, metabolism or degradation of carbohydrates  
PT in the plant grain useful in generating plants having improved  
PT nutritional properties.

XX Claim 2; SEQ ID NO 73; 130pp; English.

XX This invention, in the area of plant biotechnology, relates to novel  
CC polynucleotides comprising a nucleotide sequence encoding a protein which  
CC is involved in or associated with the synthesis, metabolism or  
CC degradation of carbohydrates in the plant grain and the expression of  
CC which is up-regulated during grain filling. The plant is selected from  
CC corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,  
CC sugarcane, wheat, and rice. The invention may be useful for the  
CC improvement of protein, oil, starch, fibre and moisture content of the  
CC cereal grains. In addition, carbohydrate levels may be modified to a more  
CC desirable level using the present invention. The present sequence is a  
CC DNA sequence encoding a rice protein of the invention. Note: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC ftp.wipo.int/pub/publishedpct\_sequences.

XX Sequence 2307 BP; 608 A; 465 C; 620 G; 614 T; 0 U; 0 Other;

XX Query Match 9.3%; Score 124.4; DB 9; Length 2307;  
Best Local Similarity 86.7%; Pred. No. 7e-28;  
Matches 137; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 263 GTTATGACATCTGAGACACAGTATGTTTCACGGAACATGAGAAAGATGATCATC 322  
DB 2004 GTTATGACATCTGAGACACAGTATGTTTCGGAACATGAGAAAGATGATCATC 2063

QY 323 CCTCAAAGAGAGATTGTTGTTTTCACCTTCACCTGAGACATAGTTTTCAC 382  
DB 2064 CTTCGAGAGAGAGATTGTTGTTTTCACCTTCACCTGAGATATAGCTATTTCGA 2123

QY 383 CTACCGTGTGGGTTCACAGCTCGGAGATACAAAG 420  
DB 2124 CTATCGCGTGGTGTGTTTAAAGCTCGGAAGATACAAAG 2161

RESULT 12

AAZ99941  
ID AAZ99941 standard; DNA; 1120 BP.

XX AAZ99941;

DT 25-JUL-2000 (first entry)

DE Nucleotide sequence of starch branching enzyme II clone B10.

XX Wheat; starch branching enzyme II; SBEII; SBEII-1; starch; SBEII-2;  
KW gelatinisation onset; transgenic plant; foodstuff; bakery product; ss.

XX Triticum aestivum.

XX WO200015810-A1.

XX 23-MAR-2000.

XX 09-SEP-1999; 99WO-GB003011.

XX 10-SEP-1998; 98EP-00307337.

XX (PLAN-) PLANT BREEDING INT CAMBRIDGE LTD.

XX Goldsbrough A, Colliver S;  
XX  
XX WPI, 2000-271446/23.  
XX

XX DNA encoding wheat starch branching enzyme II isoforms, useful in  
XX altering the characteristics of a plant, especially elevated starch  
XX gelatinization onset and/or peak temperature.  
XX

PS Claim 4; Page 123-124; 197pp; English.

XX The present sequence represents a clone of wheat starch branching enzyme  
XX II (SBEII), which is part of a novel subclass of known SBEII genes,  
XX designated SBEII-1, subclass B. The specification also describes subclass  
XX SBEII-2 sequences. The SBEII-1 genes are thought to have similar  
XX functional properties to the maize SBEIIb gene. Starch branching enzymes  
XX catalyze the formation of the alpha-1,6 linkages, creating branch points  
XX in the growing starch molecule, via hydrolysis of an alpha-1,4 linkage  
XX followed by reattachment of the released alpha-1,4-glucan chain to the  
XX same or another glucosyl chain. SBEII polypeptides can be used to alter  
XX the characteristics of a plant, in particular to alter starch so that it  
XX has an elevated gelatinisation onset and/or peak temperature. Starch  
XX obtained from transgenic plants is useful in the preparation or  
XX processing a foodstuff, particularly bakery products  
XX

SQ Sequence 1120 BP; 338 A; 208 C; 252 G; 308 T; 0 U; 14 Other;

Query Match 9.2%; Score 124.2; DB 3; Length 1120;

Best Local Similarity 79.5%; Pred. No. 5.2e-28;

Matches 147; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 264 TTTATGACATCTGAGCACCAGTATGTTTCACGGAACATGAGAAATAGGTATATC 323

DB 325 TTTATGACATCAACACCCAGTATGTTTCGGAACATGAGAAATAGGTATATC 384

QY 324 CTCGAAAGAGAGATTGGTATGTTTTCACCTTCACCTGAGCAATAGCTTTTGGAC 383

DB 385 TTGAAAAAGGGGACTGTGATTTGTTCACTTCAGTAGATGATATTTCGAC 444

QY 384 TACCGTGTGGGTGTTCCAGCTGAGAGTACAGATAGTCTGCTTTTATTGTC 443

DB 445 TACCGGTGCTGTTTAAAGCTGGAGATGAGTGTAGACTCGAGCGCTGGA 504

QY 444 CCCTT 448

DB 505 CTCTT 509

RESULT 13

AAZ99940 standard; DNA; 1087 BP.

AAZ99940;

25-JUL-2000 (first entry)

Nucleotide sequence of starch branching enzyme II clone B4.

Wheat; starch branching enzyme II; SBEII; SBEII-1; starch; SBEII-2;

gelatinisation onset; transgenic plant; foodstuff; bakery product; ss.

Triticum aestivum.

WO200015810-A1.

23-MAR-2000.

09-SEP-1999; 99WO-GB003011.

10-SEP-1998; 98EP-00307337.

(PLAN-) PLANT BREEDING INT CAMBRIDGE LTD.

PI Goldsbrough A, Colliver S;  
XX  
XX WPI, 2000-271446/23.  
XX

XX DNA encoding wheat starch branching enzyme II isoforms, useful in  
XX altering the characteristics of a plant, especially elevated starch  
XX gelatinization onset and/or peak temperature.  
XX

PS Claim 3; Page 123; 197pp; English.

XX The present sequence represents a clone of wheat starch branching enzyme  
XX II (SBEII), which is part of a novel subclass of known SBEII genes,  
XX designated SBEII-1, subclass C. The specification also describes subclass  
XX SBEII-2 sequences. The SBEII-1 genes are thought to have similar  
XX functional properties to the maize SBEIIb gene. Starch branching enzymes  
XX catalyze the formation of the alpha-1,6 linkages, creating branch points  
XX in the growing starch molecule, via hydrolysis of an alpha-1,4 linkage  
XX followed by reattachment of the released alpha-1,4-glucan chain to the  
XX same or another glucosyl chain. SBEII polypeptides can be used to alter  
XX the characteristics of a plant, in particular to alter starch so that it  
XX has an elevated gelatinisation onset and/or peak temperature. Starch  
XX obtained from transgenic plants is useful in the preparation or  
XX processing a foodstuff, particularly bakery products  
XX

SQ Sequence 1087 BP; 336 A; 214 C; 235 G; 296 T; 0 U; 6 Other;

Query Match 9.2%; Score 124; DB 3; Length 1087;

Best Local Similarity 84.8%; Pred. No. 5.9e-28;

Matches 139; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 264 TTTATGACATCTGAGCACCAGTATGTTTCACGGAACATGAGAAATAGGTATATC 323

DB 325 TTTATGACATCAACACCCAGTATGTTTCGGAACATGAGAAATAGGTATATC 384

QY 324 CTCGAAAGAGAGATTGGTATGTTTTCACCTTCACCTGAGCAATAGCTTTTGGAC 383

DB 385 TTGAAAAAGGGGACTGTGATTTGTTCACTTCAGTAGATGATATTTCGAC 444

QY 384 TACCGTGTGGGTGTTCCAGCTGAGAGTACAGATAGTCTT 427

DB 445 TACCGGTGCTGTTTAAAGCTGGAGATGAGTGTGCTT 488

RESULT 14

ADC08218 standard; DNA; 2304 BP.

ADC08218;

18-DEC-2003 (first entry)

Rice DNA sequence Seq ID523 related to grain filling.

plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;

carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;

tomato; banana; cotton; peanut; sorghum; tobacco; sugarcane;

wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;

gene; ds; plant.

Oryza sativa.

WO200300905-A2.

03-JAN-2003.

21-JUN-2002; 2002WO-1B002450.

22-JUN-2001; 2001US-0300112P.

26-SEP-2001; 2001US-0325277P.

20-DEC-2001; 2001US-0342327P.

(SYGN) SYNGENTA PARTICIPATIONS AG.





GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 10, 2004, 03:15:35 ; Search time 95.5669 Seconds  
(without alignments)

7804.525 Million cell updates/sec

Title: US-09-508-377-10\_COPY\_10120\_11463  
Perfect score: 1344  
Sequence: 1 ttatagatcgtgctgtaacaa.....tcgctcgaacgtgaatacc 1344

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA: \*  
1: /cgn2\_6/prodata/2/ina/5A\_COMB.seq: \*  
2: /cgn2\_6/prodata/2/ina/5B\_COMB.seq: \*  
3: /cgn2\_6/prodata/2/ina/6A\_COMB.seq: \*  
4: /cgn2\_6/prodata/2/ina/6B\_COMB.seq: \*  
5: /cgn2\_6/prodata/2/ina/6C\_COMB.seq: \*  
6: /cgn2\_6/prodata/2/ina/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	370	27.5	2853	4	US-09-609-040-3
2	125.6	9.3	2446	4	US-09-731-166-9
3	120.6	9.0	2665	4	US-09-257-894-1
4	120.6	9.0	2720	4	US-09-731-166-11
5	120.6	9.0	2725	3	US-08-941-445A-14
6	91	6.8	3074	3	US-09-087-277-1
7	91	6.8	3074	4	US-09-658-499-1
8	58.4	4.3	2487	4	US-09-257-894-19
9	58.4	4.3	2565	4	US-09-257-894-24
10	58.4	4.3	2763	3	US-08-941-445A-16
11	58.4	4.3	2772	4	US-09-257-894-12
12	55.4	4.1	414	4	US-09-257-894-2
13	55.4	4.1	2909	3	US-08-104-158-1
14	54	4.0	2909	3	US-09-609-040-1
15	54	4.0	3128	3	US-08-716-449-1
16	54	3.9	2087	4	US-09-257-894-9
17	52	3.9	2165	4	US-09-257-894-8
18	44	3.3	7218	1	US-08-232-463-14
19	44	3.3	832	4	US-09-621-976-1813
20	37.2	2.8	1230025	4	US-09-198-452A-1
21	37.2	2.8	746	3	US-09-328-111-105
22	35	2.6	7218	1	US-08-232-463-14
23	34.8	2.6	164976	4	US-08-916-421B-1
24	34.6	2.5	21784	4	US-09-820-002-3
25	32.8	2.4	632	3	US-09-385-982-177
26	32.8	2.4	99916	4	US-09-816-095-3
27	32.8	2.4	99916	4	US-09-816-095-3

c	28	32.2	2.4	848	3	US-08-905-223-27	Sequence 27, Appl
c	29	32.2	2.4	848	4	US-09-247-155-27	Sequence 27, Appl
c	30	32.2	2.4	848	4	US-09-663-600A-27	Sequence 27, Appl
c	31	32.2	2.4	848	4	US-09-621-976-5	Sequence 5, Appl
c	32	32.2	2.4	28171	4	US-08-961-527-22	Sequence 22, Appl
c	33	32	2.4	2448	3	US-08-691-563C-53	Sequence 53, Appl
c	34	32	2.4	2448	4	US-09-374-766-53	Sequence 53, Appl
c	35	32	2.4	2448	4	US-08-979-847B-49	Sequence 49, Appl
c	36	32	2.4	22846	2	US-08-468-461-3	Sequence 3, Appl
c	37	32	2.4	22846	3	US-07-890-609-3	Sequence 3, Appl
c	38	32	2.4	640681	4	US-09-790-988-1	Sequence 1, Appl
c	39	31.8	2.4	234	4	US-09-107-532A-252	Sequence 252, App
c	40	31.8	2.4	364	4	US-09-621-976-17202	Sequence 17202, A
c	41	31.8	2.4	474	4	US-09-621-976-18033	Sequence 18033, A
c	42	31.8	2.4	796	4	US-08-956-171E-602	Sequence 602, App
c	43	31.8	2.4	1429	2	US-09-185-385-4	Sequence 4, Appl
c	44	31.8	2.4	1429	3	US-09-185-277-4	Sequence 4, Appl
c	45	31.8	2.4	1497	4	US-09-220-132-94	Sequence 94, Appl

## ALIGNMENTS

RESULT 1  
US-09-609-040-3  
Sequence 3, Application US/09609040  
Patent No. 6570066  
GENERAL INFORMATION:  
APPLICANT: Willmitzer, et al.  
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING ENZYMES THAT ALTER THE CARBOHYDRATE  
TITLE OF INVENTION: CONCENTRATION AND COMPOSITION IN PLANTS  
FILE REFERENCE: 514413-3515.1  
CURRENT FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: PCT/EP92/00302  
PRIOR FILING DATE: 1992-02-11  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 3  
LENGTH: 2853  
TYPE: DNA  
ORGANISM: Trifolium aestivum  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (313)..(2499)  
OTHER INFORMATION: BRANCHING ENZYME  
US-09-609-040-3

Query Match 27.5%; Score 370; DB 4; Length 2853;  
Best Local Similarity 100.0%; Pred. No. 8.6e-110; Index 0; Gaps 0;  
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
c 961 GAACATCCGATGACACAGCGCGCTCTTTCTGGTGTACACTCCGACAGACTGCG 1020  
c 2419 GAACATCCGATGACACAGCGCGCTCTTTCTGGTGTACACTCCGACAGACTGCG 2478  
c 1021 GTGCTGTATGCCCTTACAGAGTAACACAGAGCGCTTTTACAGAGCAAGAGAA 1080  
c 2479 GTGCTGTATGCCCTTACAGAGTAACACAGAGCGCTTTTACAGAGCAAGAGAA 2538  
c 1081 CTCGAGAGAGCTCGTGATTCGAGACGAGCGGCGAGGCTCTCTCAAG 1140  
c 2539 CTCGAGAGAGCTCGTGATTCGAGACGAGCGGCGAGGCTCTCTCAAG 2598  
c 1141 CGCCATGACTGGAGAGGAGTGTGCTCTTCCCAAGTCCAGAGAGCAGATGATAG 1200  
c 2599 CGCCATGACTGGAGAGGAGTGTGCTCTTCCCAAGTCCAGAGAGCAGATGATAG 2658  
c 1201 GTAGCTTTGGTGTAGCGCTCGAAAGAAATGAGAGGCGCTGGGTCTTTGTCTGCA 1260  
c 2659 GTAGCTTTGGTGTAGCGCTCGAAAGAAATGAGAGGCGCTGGGTCTTTGTCTGCA 2718  
c 1261 CTGAACCTCTCTATCTGTGACATCCCGGCTGTTTGTACATATACTAATATG 1320

Db 2719 CTGACCTCTCTCTATCTTGACATTCGGGTGTTTGTGACATATACATTAATTG 2778  
QY 1321 CCCGTGGCCT 1330  
Db 2779 CCCGTGGCCT 2788

RESULT 2  
US-09-731-166-9

Sequence 9, Application US/09731166  
Patent No. 6639126  
GENERAL INFORMATION:  
APPLICANT: Sewalt, Vincent J. H.  
TITLE OF INVENTION: Production of Modified Polysaccharides  
FILE REFERENCE: 35718/206348  
CURRENT APPLICATION NUMBER: US/09/731.166  
CURRENT FILING DATE: 2000-12-06  
PRIORITY APPLICATION NUMBER: 60/169,993  
PRIORITY FILING DATE: 1999-12-06  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 9  
LENGTH: 2446  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (0)..(0)  
OTHER INFORMATION: SBE11a  
OTHER INFORMATION: Genbank Accession No. 6639126 U65948  
NAME/KEY: CDS  
LOCATION: (2)..(2446)  
US-09-731-166-9

Query Match 9.3%; Score 125.6; DB 4; Length 2446;  
Best Local Similarity 79.3%; Pred. No. 3.5e-30;  
Matches 149; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 262 AGTTTATGACATCTGAGCAGCAGATGTTTCAAGGAAATGAGAAAGTAAGGATGATCA 321  
Db 2118 AATTCATGACATCTGATGATCATATGATATCAAGGAAATGAGAAAGTAAGGATGATCA 2177  
QY 322 TCCCTCAAAAGAGAGATTGGTATTGTTTCAACTTCCACTGGAGCAATAGCTTTTGG 381  
Db 2178 TCTTTGAGAGAGAGATTGGTATTGTTTCAACTTCCACTGGAGCAATAGCTTTTGG 2237  
QY 382 ACTACCGGTGGGGGTGTTCCAAAGCTGGAGAGTACAGGATAGCTTGCCTTTTCATTTGTC 441  
Db 2238 ACTATCGGTTGGTTGTTTCAAGCTGGAGAGTACAGGATAGCTTGAATTTCTGAGAGTG 2297  
QY 442 CACCTTC 449  
Db 2298 GCTTTTC 2305

RESULT 3  
US-09-257-894-1  
Sequence 1, Application US/09257894  
Patent No. 6376749  
GENERAL INFORMATION:  
APPLICANT: Broglie, Karen E.  
APPLICANT: Klein, Theodore W.  
APPLICANT: Hubbard, Nathalie L.  
APPLICANT: Lightner, Jonathan E.  
TITLE OF INVENTION: No. 6376749el Starches via Modification of  
TITLE OF INVENTION: Expression of Starch Biosynthesis  
TITLE OF INVENTION: Erythre Genes  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: E. I. du Pont de Nemours and Company  
STREET: 1007 Market Street

CITY: Wilmington  
STATE: Delaware  
COUNTRY: USA  
ZIP: 19898  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Microsoft Windows 95  
SOFTWARE: Version 7.0A  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/257,894  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 09/091,052  
FILING DATE: JUNE 10, 1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Majarian, William R.  
REGISTRATION NUMBER: 41,173  
REFERENCE/DOCKET NUMBER: BB-1066-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 302-992-4926  
TELEFAX: 302-773-0164

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2665 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 79..2476  
US-09-257-894-1

Query Match 9.0%; Score 120.6; DB 4; Length 2665;  
Best Local Similarity 82.6%; Pred. No. 1.6e-28;  
Matches 138; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 262 AGTTTATGACATCTGAGCAGCAGATGTTTCAAGGAAATGAGAAAGTAAGGATGATCA 321  
Db 2162 AATTCATGACATCTGATGATCATATGATATCCGGAACATGAGAGAGATAGGATG 2221  
QY 322 TCCCTCAAAAGAGAGATTGGTATTGTTTCAACTTCCACTGGAGCAATAGCTTTTGG 381  
Db 2222 TCTTTGAGAGAGAGATTGGTATTGTTTCAACTTCCACTGGAGCAATAGCTTTTGG 2281  
QY 382 ACTACCGGTGGGGGTGTTCCAAAGCTGGAGAGTACAGGATAGCTTGCCTTTTCATTTGTC 428  
Db 2282 ACTACCGTATGTTGTTGTCGAAAGCTGGAGTATAGAGTGTGTTG 2328

RESULT 4  
US-09-731-166-11  
Sequence 11, Application US/09731166  
Patent No. 6639126  
GENERAL INFORMATION:  
APPLICANT: Sewalt, Vincent J. H.  
APPLICANT: Singletary, George W.  
TITLE OF INVENTION: Production of Modified Polysaccharides  
FILE REFERENCE: 35718/206348  
CURRENT APPLICATION NUMBER: US/09/731.166  
CURRENT FILING DATE: 2000-12-06  
PRIORITY APPLICATION NUMBER: 60/169,993  
PRIORITY FILING DATE: 1999-12-06  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 11  
LENGTH: 2720  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
NAME/KEY: misc\_feature

LOCATION: (0)...(0)  
OTHER INFORMATION: SBEID  
OTHER INFORMATION: Genbank Accession No. 6639126 AF072725  
NAME/KEY: CDS  
LOCATION: (101)...(2500)  
US-09-731-166-11

Query Match 9.0%; Score 120.6; DB 4; Length 2720;  
Best Local Similarity 82.6%; Pred. No. 1.6e-28;  
Matches 138; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 262 AGTTATGACATCTGAGCAGCATGTTGTTTCCAGGAAATAGAGAAATAGGTATCA 321  
DB 2184 AATTCATGACATCTGATCAACGATATTTCCCGAATAGAGAGATTAAGGTATG 2243  
QY 322 TCCTCAAAAGAGAGATTTGGTATTTGTTTCAACTTCAGTGAACAATAGCTTTTGG 381  
DB 2244 TGTTCGAAAAGGAGATTTGGTATTTGTTTCAACTTCAGTGAACAATAGCTATTTG 2303  
QY 382 ACTACCGTGTGGGTGTTCCAGCCTGGAGATCAAGGTATGCTTG 428  
DB 2304 ACTACCGTATTTGTTGTGCAAAAGCCTGGGATGATTAAGGTGCTTG 2350

## RESULT 5

US-08-941-445A-14  
Sequence 14, Application US/08941445A  
Patent No. 6107060  
GENERAL INFORMATION:  
APPLICANT: Keeling, Peter  
APPLICANT: Guan, Hanning  
TITLE OF INVENTION: Starch Encapsulation  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
STREET: 5370 Manhattan Circle  
CITY: Boulder  
STATE: CO  
COUNTRY: US  
ZIP: 80303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/941,445A  
FILING DATE: 30-SEP-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/026,855  
FILING DATE: 30-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Winner, Ellen P  
REGISTRATION NUMBER: 28,547  
REFERENCE/DOCKET NUMBER: 89-97  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 499-8080  
TELEFAX: (303) 499-8089  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2725 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: not relevant  
MOLECULE TYPE: mRNA  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Zea mays  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 91..264  
FEATURE:

NAME/KEY: mat\_peptide  
LOCATION: 265..2487  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 91..2490  
US-08-941-445A-14

Query Match 9.0%; Score 120.6; DB 3; Length 2725;  
Best Local Similarity 82.6%; Pred. No. 1.6e-28;  
Matches 138; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 262 AGTTATGACATCTGAGCAGCATGTTGTTTCCAGGAAATAGAGAAATAGGTATCA 321  
DB 2174 AATTCATGACATCTGATCAACGATATTTCCCGAATAGAGAGATTAAGGTATG 2233  
QY 322 TCCTCAAAAGAGAGATTTGGTATTTGTTTCAACTTCAGTGAACAATAGCTTTTGG 381  
DB 2234 TGTTCGAAAAGGAGATTTGGTATTTGTTTCAACTTCAGTGAACAATAGCTATTTG 2293  
QY 382 ACTACCGTGTGGGTGTTCCAGCCTGGGAGTCAAGGTATGCTTG 428  
DB 2294 ACTACCGTATTTGTTGTGCAAAAGCCTGGGATGATTAAGGTGCTTG 2340

## RESULT 6

US-09-087-277-1  
Sequence 1, Application US/09087277B  
Patent No. 6169226  
GENERAL INFORMATION:  
APPLICANT: EK, Bo  
APPLICANT: KHOSNODI, Jamsheed  
APPLICANT: LARSSON, Claes-Tomas  
APPLICANT: LARSSON, Hakan  
TITLE OF INVENTION: SPARCH BRANCHING ENZYME II OF POTATO  
FILE REFERENCE: 003300-486  
CURRENT APPLICATION NUMBER: US/09/087,277B  
CURRENT FILING DATE: 1998-05-29  
EARLIER APPLICATION NUMBER: PCT/SE96/01558  
EARLIER FILING DATE: 1996-11-28  
EARLIER APPLICATION NUMBER: SE 9504272-7  
EARLIER FILING DATE: 1995-11-29  
EARLIER APPLICATION NUMBER: SE 9601506-0  
EARLIER FILING DATE: 1996-04-19  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 1  
LENGTH: 3074  
TYPE: DNA  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Description of Unknown Organism: bell gene  
OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum  
OTHER INFORMATION: (potato)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (189)..(2825)  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: (189)..(332)  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: (333)..(2825)  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (92)..(2156)  
OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are  
OTHER INFORMATION: n wherein n = A, C, G or T.  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (285)..(287)  
OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu, Val  
OTHER INFORMATION: or Phe.

FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1404)..(1406)  
OTHER INFORMATION: Amino acid 358 is Xaa wherein Xaa = Leu or Phe.  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1428)..(1430)  
OTHER INFORMATION: Amino acid 366 is Xaa wherein Xaa = Thr.  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1896)..(1898)  
OTHER INFORMATION: Amino acid 522 is Xaa wherein Xaa = Tyr, Ser, Cys  
OTHER INFORMATION: or Phe.  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (2154)..(2156)  
OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro.  
US-09-087-277-1

Query Match  
Best Local Similarity 67.8%; Pred. No. 7.8e-19; Length 3074;  
Matches 127; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 262 AGTTATGACATCTGAGCACCAGTATGTTTCACGAAACATGAGGAAGATAGGTATCA 321  
DB 2449 AGTTATGACCTCAGAACACAGTTCATATCAGAAAGATGAGAGATAGATGATG 2508  
QY 322 TCCTCAAAAGAGAGATTTGATTTTTCACACTCCACTGAGCATAGCTTTTTC 381  
DB 2509 TATTTGAAAAAGGAAACCTAGTTTTCCTTTAATTTTCACTGACAAAAAGCTATTTCAG 2568  
QY 382 ACTACCGTGTGGGTGTTCCAGGCTGGAGTACAGAGTATGCTTTCATTGTC 441  
DB 2569 ACTATGCGATAGGCTGCTGAAAGCTGGAATAATCAAGTTGCTTGACTCAGATGATC 2628  
QY 442 CACCTT 448  
DB 2629 CACTTT 2635

RESULT 7  
US-09-658-499-1  
Sequence 1, Application US/09658499  
Patent No. 6469231  
GENERAL INFORMATION:  
APPLICANT: EK, BO  
APPLICANT: KHOSNOODI, Jamshid  
APPLICANT: LARSSON, Claes-Tomas  
APPLICANT: LARSSON, Hakan  
APPLICANT: RASK, Lars  
TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO  
FILE REFERENCE: 003300-486  
CURRENT APPLICATION NUMBER: US/09/658,499  
CURRENT FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 09/087,277  
PRIOR FILING DATE: 1998-05-29  
PRIOR APPLICATION NUMBER: PCT/SE96/01558  
PRIOR FILING DATE: 1996-11-28  
PRIOR APPLICATION NUMBER: SE 9504272-7  
PRIOR FILING DATE: 1995-11-29  
PRIOR APPLICATION NUMBER: SE 9601506-0  
PRIOR FILING DATE: 1996-04-19  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 3074  
TYPE: DNA  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Description of Unknown Organism: bell gene  
OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum  
OTHER INFORMATION: (potato)  
NAME/KEY: CDS

LOCATION: (189)..(2825)  
NAME/KEY: sig\_peptide  
LOCATION: (189)..(332)  
NAME/KEY: mat\_peptide  
LOCATION: (333)..(2825)  
NAME/KEY: misc\_feature  
LOCATION: (92)..(2156)  
OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are  
OTHER INFORMATION: n wherein n = A, C, G or T.  
NAME/KEY: misc feature  
LOCATION: (285)..(287)  
OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu, Val  
OTHER INFORMATION: or Phe.  
NAME/KEY: misc feature  
LOCATION: (1404)..(1406)  
OTHER INFORMATION: Amino acid 358 is Xaa wherein Xaa = Leu or Phe.  
NAME/KEY: misc feature  
LOCATION: (1428)..(1430)  
OTHER INFORMATION: Amino acid 366 is Xaa wherein Xaa = Thr.  
NAME/KEY: misc feature  
LOCATION: (1896)..(1898)  
OTHER INFORMATION: Amino acid 522 is Xaa wherein Xaa = Tyr, Ser, Cys  
OTHER INFORMATION: or Phe.  
NAME/KEY: misc feature  
LOCATION: (2154)..(2156)  
OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro.  
US-09-658-499-1

Query Match  
Best Local Similarity 67.9%; Pred. No. 7.8e-19; Length 3074;  
Matches 127; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 262 AGTTATGACATCTGAGCACCAGTATGTTTCACGAAACATGAGGAAGATAGGTATCA 321  
DB 2449 AGTTATGACCTCAGAACACAGTTCATATCAGAAAGATGAGAGATAGATGATG 2508  
QY 322 TCCTCAAAAGAGAGATTTGATTTTTCACACTCCACTGAGCATAGCTTTTTC 381  
DB 2509 TATTTGAAAAAGGAAACCTAGTTTTCCTTTAATTTTCACTGACAAAAAGCTATTTCAG 2568  
QY 382 ACTACCGTGTGGGTGTTCCAGGCTGGAGTACAGAGTATGCTTTCATTGTC 441  
DB 2569 ACTATGCGATAGGCTGCTGAAAGCTGGAATAATCAAGTTGCTTGACTCAGATGATC 2628  
QY 442 CACCTT 448  
DB 2629 CACTTT 2635

RESULT 8  
US-09-731-166-13  
Sequence 13, Application US/09731166  
Patent No. 6639126  
GENERAL INFORMATION:  
APPLICANT: Sewalt, Vincent J. H.  
APPLICANT: Singletary, George W.  
TITLE OF INVENTION: Production of Modified Polysaccharides  
FILE REFERENCE: 35718/206348  
CURRENT APPLICATION NUMBER: US/09/731,166  
CURRENT FILING DATE: 2000-12-06  
PRIOR APPLICATION NUMBER: 60/169,993  
PRIOR FILING DATE: 1999-12-06  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13  
LENGTH: 2470  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (0)..(0)  
OTHER INFORMATION: SBE1 -- Genbank Accession No. 6639126 217959  
NAME/KEY: CDS

LOCATION: (2)...(2470)  
US-09-731-166-13

Query Match 4.3%; Score 58.4; DB 4; Length 2470;  
Best Local Similarity 56.9%; Pred. No. 2.8e-08;  
Matches 107; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 301 ATGAGAGATTAAGTGTATCATCTCAAAAGAGAGATTGGTATTGTTTCAACTTCC 360  
DB 1995 ACGATGAGAGAAAGGTTATGTCTTGAACGTGAGATTAGTTTGTTCATTCC 2054  
QY 361 ACTGAGCAATPAGCTTTTGTACTACCGTGTGGGTTCAGCTGGGAAGTACAAG 420  
DB 2055 ATCCCAAGAAACCTTACGAGGGCTCAAAAGTGGATGCGATTGCTGGGAAATACAGAG 2114  
QY 421 TATGCTTGCCTTTTATTTGTCACCCCTTACCAAGTATGAGTGGGGCTTCTCAACT 480  
DB 2115 TAGCCCTGACTCTGATGCTGTGCTTGGTGGACATGGAAGATTGGCCACGACTGG 2174  
QY 481 TTTAATTC 488  
DB 2175 ATCACTTC 2182

## RESULT 9

US-09-257-894-19/c  
Sequence 19, Application US/09257894  
Patent No. 6376749

GENERAL INFORMATION:  
APPLICANT: Broglie, Karen E.  
APPLICANT: Klein, Theodore M.  
APPLICANT: Hubbard, Natalie L.  
APPLICANT: Lightner, Jonathan E.  
TITLE OF INVENTION: No. 6376749el Starches via Modification of  
TITLE OF INVENTION: Expression of Starch Biosynthesis  
NUMBER OF INVENTION: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: E. I. du Pont de Nemours and Company  
STREET: 1007 Market Street  
CITY: Wilmington  
STATE: Delaware  
COUNTRY: USA  
ZIP: 19898

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Microsoft Windows 95  
SOFTWARE: Version 7.0A  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/257,894  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/091,052  
FILING DATE: JUNE 10, 1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Majarian, William R.  
REGISTRATION NUMBER: 41,173  
REFERENCE/DOCKET NUMBER: BB-1066-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 302-992-4926  
TELEFAX: 302-773-0164

INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2487 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-09-257-894-19

Query Match

4.3%; Score 58.4; DB 4; Length 2487;

Best Local Similarity 56.9%; Pred. No. 2.8e-08;  
Matches 107; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 301 ATGAGAGATTAAGTGTATCATCTCAAAAGAGAGATTGGTATTGTTTCAACTTCC 360  
DB 380 ACGATGAGAGAAAGGTTATGTCTTGAACGTGAGATTAGTTTGTTCATTCC 321  
QY 361 ACTGAGCAATPAGCTTTTGTACTACCGTGTGGGTTCAGCTGGGAAGTACAAG 420  
DB 320 ATCCCAAGAAACCTTACGAGGGCTCAAAAGTGGATGCGATTGCTGGGAAATACAGAG 261  
QY 421 TATGCTTGCCTTTTATTTGTCACCCCTTACCAAGTATGAGTGGGGCTTCTCAACT 480  
DB 260 TAGCCCTGACTCTGATGCTGTGCTTGGTGGACATGGAAGATTGGCCACGACTGG 201  
QY 481 TTTAATTC 488  
DB 200 ATCACTTC 193

## RESULT 10

US-09-257-894-24  
Sequence 24, Application US/09257894  
Patent No. 6376749

GENERAL INFORMATION:  
APPLICANT: Broglie, Karen E.  
APPLICANT: Klein, Theodore M.  
APPLICANT: Hubbard, Natalie L.  
APPLICANT: Lightner, Jonathan E.  
TITLE OF INVENTION: No. 6376749el Starches via Modification of  
TITLE OF INVENTION: Expression of Starch Biosynthesis  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: E. I. du Pont de Nemours and Company  
STREET: 1007 Market Street  
CITY: Wilmington  
STATE: Delaware  
COUNTRY: USA  
ZIP: 19898

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Microsoft Windows 95  
SOFTWARE: Version 7.0A  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/257,894  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/091,052  
FILING DATE: JUNE 10, 1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Majarian, William R.  
REGISTRATION NUMBER: 41,173  
REFERENCE/DOCKET NUMBER: BB-1066-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 302-992-4926  
TELEFAX: 302-773-0164

INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2565 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-09-257-894-24

Query Match 4.3%; Score 58.4; DB 4; Length 2565;  
Best Local Similarity 56.9%; Pred. No. 2.9e-08;  
Matches 107; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 301 ATGAGAGATTAAGTGTATCATCTCAAAAGAGAGATTGGTATTGTTTCAACTTCC 360

Db 1997 ACCATAGAGAAAGTATGCTTTTGAAGTGAGATTGATTTGTTTCAATTCC 2056  
QY 361 ACTGAGACATAGCTTTTGTGACTACGCGTGTGGGTGTTCCAGCCTGGAGTACAGG 420  
Db 2057 ATCCCAAGAAACTTACGAGGCTACAAAGTGGATGCGATTGCTGGAAATACAGG 2116  
QY 421 TATGCTTGCTTTTCAATTGTCACCTTTCACCAAGTGGATTAGTGGGCTTTTCAACT 480  
Db 2117 TAGCCCTGAGACTGTGATGCTGTGTCTTCCGTGACATGAGAGATTGGCCAGCAGCTGG 2176  
QY 481 TTTAATTC 488  
Db 2177 ATCACTTC 2184

RESULT 11  
US-08-941-445A-16  
Sequence 16, Application US/08941445A  
Patent No. 6107060  
GENERAL INFORMATION:  
APPLICANT: Keeling, Peter  
TITLE OF INVENTION: Search Encapsulation  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
STREET: 5370 Manhattan Circle  
CITY: Boulder  
STATE: CO  
COUNTRY: US  
ZIP: 80303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/941,445A  
FILING DATE: 30-SEP-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/026,855  
FILING DATE: 30-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Winner, Ellen P  
REGISTRATION NUMBER: 28,547  
REFERENCE/DOCKET NUMBER: 89-97  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 499-8080  
TELEFAX: (303) 499-8089  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2763 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: not relevant  
MOLECULE TYPE: mRNA  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Zea mays  
FEATURE:  
NAME/KEY: translt\_peptide  
LOCATION: 2..190  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 191..2467  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 2..2470  
US-08-941-445A-16

Query Match 4.3%; Score 58.4; DB 3; Length 2763;

Best Local Similarity 56.9%; Pred. No. 3.1e-08;  
Matches 107; Conservative 0; Mismatches 81; Indels 0; Gaps 0;  
QY 301 ATGAGAGAGATAGGTGATCATCTCAAAAGAGAGATTTGGTATTTGTTTCAACTCC 360  
Db 1995 ACGATGAGAGAAAGTATATGTCTTTGAACGTGGAGATTAGTTTGTTCATTTCC 2054  
QY 361 ACTGAGCAATAGCTTTTGTACTACCTGTTGGTGTTCACAGCTGGAGTACAGG 420  
Db 2055 ATCCCAAGAAACTTACGAGGCTACAAAGTGGATGCGATTTGCCGGGAAATACAGG 2114  
QY 421 TATGCTTGCTTTTCAATTGTCACCTTTCACCAAGTGGATTAGTGGGCGCTTCAACT 480  
Db 2115 TAGCCCTGAGACTGTGATGCTGTGTCTTCCGTGACATGAGAGATTGGCCAGCAGCTGG 2174  
QY 481 TTTAATTC 488  
Db 2175 ATCACTTC 2182

RESULT 12  
US-09-257-894-12  
Sequence 12, Application US/09257894  
Patent No. 6376749  
GENERAL INFORMATION:  
APPLICANT: Broglie, Karen E.  
APPLICANT: Klein, Theodore M.  
APPLICANT: Hubbard, Natalie L.  
APPLICANT: Lightner, Jonathan E.  
TITLE OF INVENTION: No. 6376749el Starches via Modification of  
TITLE OF INVENTION: Expression of Starch Biosynthesis  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: E. I. du Pont de Nemours and Company  
STREET: 1007 Market Street  
CITY: Wilmington  
STATE: Delaware  
COUNTRY: USA  
ZIP: 19898  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Microsoft Windows 95  
SOFTWARE: Version 7.0A  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/257,894  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/091,052  
FILING DATE: JUNE 10, 1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Majarian, William R.  
REGISTRATION NUMBER: 41,173  
REFERENCE/DOCKET NUMBER: BB-1066-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 302-773-0164  
TELEFAX: 302-992-4926  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2772 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 49..2580  
US-09-257-894-12

Query Match 4.3%; Score 58.4; DB 4; Length 2772;  
Best Local Similarity 56.9%; Pred. No. 3.1e-08;

Matches 107; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 301 ATGAGGAATATAGTGTATCATCCCAAGAGAGATTTGGTATTTTTCACCTTCC 360  
Db 2108 ACGATGAGGAAAAGGTTATTTGCTTGAACGTGGAATTTAGTTTGTTCATTTCC 2167  
QY 361 ACTGAGCAATAGCTTTTCTGACTCCGTGTGGGTGCTTCCAAGCTGGAGATACAG 420  
Db 2168 ATCCCAAAAACTTACGAGGGCTCAAAAGTGGATGCCATTTGCTGGAAATACAG 2227  
QY 421 TATGCTTCCTTTTCTATGTCCACCTTCACCAAGAGGTTAGTGGGGCTTACACT 480  
Db 2228 TAGCCCTGAGCTGTATGTCTGTCTTCGTGACATGGAAGAGTTGGCCAGAGGTG 2287  
QY 481 TTTAATTC 488  
Db 2288 ATCACTTC 2295

## RESULT 13

US-09-257-894-2/C  
Sequence 2, Application US/09257894

GENERAL INFORMATION:  
PATENT NO. 6376749  
APPLICANT: Broglie, Karen E.  
APPLICANT: Klein, Theodore M.  
APPLICANT: Hubbard, Natalie L.  
APPLICANT: Lightner, Jonathan E.  
TITLE OF INVENTION: No. 6376749el Starches via Modification of  
TITLE OF INVENTION: Expression of Starch Biosynthesis  
TITLE OF INVENTION: Enzyme Genes  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: E. I. du Pont de Nemours and Company  
STREET: 1007 Market Street  
CITY: Wilmington  
STATE: Delaware  
COUNTRY: USA  
ZIP: 19898  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Microsoft Windows 95  
SOFTWARE: Version 7.0A  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/257,894  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/091,052  
FILING DATE: JUNE 10, 1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Majarian, William R.  
REGISTRATION NUMBER: 41,173  
REFERENCE/DOCKET NUMBER: BB-1066-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 302-992-4926  
TELEFAX: 302-773-0164  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 414 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-257-894-2

Query Match 4.1%; Score 55.4; DB 4; Length 414;  
Best Local Similarity 80.2%; Pred. No. 8.1e-08;  
Matches 65; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

348 GTTTCACCTTCACGAGCAATAGCTTTTGTACTACCGTGTGGGTTCACAGCCT 407  
|||||

Db 414 GTGTTCACCTTCACGAGCAATAGCTTTTGTACTACCGTGTGTGGAAAAGCCT 355

QY 408 GGGAGATCAAGGTATGCTTG 428  
Db 354 GGGGTGTATAGGTGTCTTG 334

## RESULT 14

US-08-104-158-1  
Sequence 1, Application US/08104158

PATENT NO. 6215042  
GENERAL INFORMATION:  
APPLICANT: Wilmlitzer, Lothar  
APPLICANT: Sonnewald, Uwe  
APPLICANT: Kossmann, Jens  
APPLICANT: Mueller-Roeder, Bernd  
APPLICANT: Visser, Richard Gerardus Franciscus  
TITLE OF INVENTION: JACOBSEN, Evert  
TITLE OF INVENTION: PLASMIDS CONTAINING DNA-SEQUENCES THAT  
TITLE OF INVENTION: CAUSE CHANGES IN THE CARBOHYDRATE CONCENTRATION AND THE  
TITLE OF INVENTION: CARBOHYDRATE COMPOSITION IN PLANTS, AS WELL AS PLANT CELLS  
TITLE OF INVENTION: AND PLANTS CONTAINING THESE PLASMIDS  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ostroienk, Faber, Gerb & Soffen  
STREET: 1180 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-8403

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/104,158  
FILING DATE: 13-AUG-1993  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP PCT/EP92/00302  
FILING DATE: 11-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P 41 04 782.6  
FILING DATE: 13-FEB-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Wellman, Edward A.  
REGISTRATION NUMBER: 24,735  
REFERENCE/DOCKET NUMBER: PA-1996 PCT (951-91)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-382-0700  
TELEFAX: 212-382-0888  
TELEX: 236925

## INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
LENGTH: 2909 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Solanum tuberosum cv. Desiree  
STRAIN: Desiree  
DEVELOPMENTAL STAGE: growing tuber  
TISSUE TYPE: tuber  
CELL TYPE: total tuber  
IMMEDIATE SOURCE:  
LIBRARY: cDNA of total tuber mRNA in pUC 19 (Hinc II)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 2..1699

Mon Apr 12 10:24:22 2004

us-09-508-377-10\_copy\_10120\_11463.rn1

Page 8

OTHER INFORMATION: /note= "for Branching enzyme I  
OTHER INFORMATION: (partial) truncated protein: 97,11 % identity to  
OTHER INFORMATION: active potato branching enzyme"  
US-08-104-158-1

Query Match 4.0%; Score 54; DB 3; Length 2909;  
Best Local Similarity 58.9%; Pred. No. 8.6e-07;  
Matches 93; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 264 TTTATACATCTGAGCACCAGTATGTTTCACGGAAACATGAGAGATAGGTATCATC 323  
DB 1866 TTCCGTCATCAGAGAAACAGATAGTAGCAGCATGATGATATATAGGTGTGTG 1925  
QY 324 CTCGAAAGAGAGATTTGGTATTTGTTTCACTTCAGCTGGAGCAATAGCTTTTGAC 383  
DB 1926 TTGAAAGTGTGACCTGTGATTTGTTTCACTTCACCCAAATTAACATACGAAAGG 1985  
QY 384 TACCGTGTGGTGTTCGAGCTGGAGATACAGGT 421  
DB 1986 TATAAGTTGATGTGACTTGCCAGGAGATACAGGT 2023

RESULT 15

US-09-609-040-1  
Sequence 1, Application US/09609040  
Patent No. 6570066

GENERAL INFORMATION:  
APPLICANT: Wilmilizer, et al.  
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING ENZYMES THAT ALTER THE CARBOHYDRATE  
FILE REFERENCE: 514413-3515.1  
CURRENT APPLICATION NUMBER: US/09/609,040  
PRIOR APPLICATION NUMBER: PCT/EP92/00302  
PRIORITY FILING DATE: 1992-02-11  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO. 1  
LENGTH: 2909  
TYPE: DNA  
ORGANISM: Solanum tuberosum  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (2)..(1699)  
OTHER INFORMATION: BRANCHING ENZYME  
US-09-609-040-1

Query Match 4.0%; Score 54; DB 4; Length 2909;  
Best Local Similarity 58.9%; Pred. No. 8.6e-07;  
Matches 93; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 264 TTTATACATCTGAGCACCAGTATGTTTCACGGAAACATGAGAGATAGGTATCATC 323  
DB 1866 TTCCGTCATCAGAGAAACAGATAGTAGCAGCATGATGATATATAGGTGTGTG 1925  
QY 324 CTCGAAAGAGAGATTTGGTATTTGTTTCACTTCAGCTGGAGCAATAGCTTTTGAC 383  
DB 1926 TTGAAAGTGTGACCTGTGATTTGTTTCACTTCACCCAAATTAACATACGAAAGG 1985  
QY 384 TACCGTGTGGTGTTCGAGCTGGAGATACAGGT 421  
DB 1986 TATAAGTTGATGTGACTTGCCAGGAGATACAGGT 2023

Search completed: April 10, 2004, 14:13:17  
Job time: 100.567 secs



Result						Description
No.	Score	Query	Match	Length	DB	
1	1333	99.2	11476	12	US-10-433-893A-3	Sequence 3, Appl1
2	370	27.5	1119	15	US-10-260-238-3410	Sequence 3410, Ap
3	263.6	19.6	2554	12	US-10-433-893A-1	Sequence 1, Appl1
4	122.6	9.1	2559	9	US-09-192-127.1	Sequence 1, Appl1
5	122.6	9.1	3039	9	US-09-192-127.3	Sequence 3, Appl1
6	122.4	9.1	1267	15	US-10-260-223-3480	Sequence 3480, Ap
7	120.6	8.9	636	15	US-10-260-233-5563	Sequence 5563, Ap
8	119.6	8.0	2780	12	US-10-433-893A-2	Sequence 2, Appl1
9	107.2	8.0	1642	15	US-10-260-238-1027	Sequence 1027, Ap
10	97	7.2	602	9	US-09-1770-10-955	Sequence 955, Ap
11	97	7.2	2418	9	US-09-838-842A-872	Sequence 872, App
12	97	7.2	2418	11	US-09-938-842A-872	Sequence 872, App
13	95.4	7.1	2529	14	US-10-056-454A-17	Sequence 17, Appl
14	92.6	6.9	2875	14	US-10-056-454A-13	Sequence 13, Appl
15	91.6	6.8	1867	12	US-10-425-114-8329	Sequence 8329, Ap

16	91.6	6.8	5164	12	US-10-424-5599-110844	Sequence 130849, App1
17	91.6	6.8	1255	14	US-10-171-008-3	Sequence 3, App1
18	91	6.8	2576	14	US-10-056-455A-16	Sequence 16, App1
19	91	6.8	2578	14	US-10-056-455A-19	Sequence 19, App1
20	91	6.8	3074	14	US-10-554-53-1	Sequence 1, App1
21	91	6.8	3231	14	US-10-056-455A-18	Sequence 18, App1
22	89.4	6.7	3003	14	US-10-056-455A-12	Sequence 12, App1
23	89.4	6.7	3033	14	US-10-056-455A-14	Sequence 14, App1
24	84.4	6.3	3359	15	US-10-393-840-264	Sequence 264, App
25	84.4	6.3	2577	9	US-09-938-842A-33	Sequence 337, App
26	84.4	6.3	2577	11	US-09-938-842A-337	Sequence 337, App
27	58.4	4.3	2324	12	US-10-425-114-32172	Sequence 32172, App
28	58.4	4.3	2551	15	US-10-397-955A-2	Sequence 2, App1
29	55.2	4.1	2913	12	US-10-335-192A-36	Sequence 36, App1
30	55.2	4.1	2913	12	US-10-342-887-442	Sequence 442, App
31	55.2	4.1	2955	9	US-09-880-107-7-2148	Sequence 2148, App
32	55.2	4.1	2955	10	US-09-918-624B-30	Sequence 30, App
33	55.2	4.1	2958	12	US-10-862-511-107	Sequence 107, App1
34	55.2	4.1	2994	14	US-10-084-817-92	Sequence 92, App1
35	55.2	4.1	3075	14	US-10-240-965-135	Sequence 135, App
36	54.8	4.1	310	14	US-10-102-524-1616	Sequence 1616, App
37	54	4.0	1380	12	US-10-424-5599-114092	Sequence 141092, App
38	53.6	3.9	2443	15	US-10-397-954A-1	Sequence 1, App1
39	53	3.9	2115	15	US-10-369-493-25407	Sequence 25407, App
40	50.4	3.8	2638	15	US-10-369-493-27563	Sequence 27563, App
41	48.6	3.6	897	12	US-10-823-114-11503	Sequence 11503, App
42	48.4	3.6	358	12	US-10-085-783A-54140	Sequence 54140, App
43	48.4	3.6	358	15	US-10-242-535A-54140	Sequence 54140, App
44	48.4	3.6	489	12	US-10-085-783-11106	Sequence 14106, App
45	48.4	3.6	489	15	US-10-242-535A-11106	Sequence 14106, App

## ALIGNMENTS

```

RESULT 1
US-10-434-893A-3
; Sequence 3, Application US/10434893A
; Publication No. US20040060083A1
GENERAL INFORMATION:
APPLICANT: Ahmed Regina
APPLICANT: Matthew Kennedy Morell
TITLE OF INVENTION: Sadequr Rahman
TITLE OF INVENTION: Barley with altered branching enzyme activity and starch and
FILE REFERENCE: 69425
CURRENT APPLICATION NUMBER: US/10/434,893A
CURRENT FILING DATE: 2003-05-09
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 2.1
SEQ ID NO 3
LENGTH: 11476
TYPE: DNA
ORGANISM: Aegilops tauschii
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)...(11476)
OTHER INFORMATION: n is a, c, g or t
FEATURE:
OTHER INFORMATION: SSBP11a gene
US-10-434-893A-3

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Query Match	Score	DB	Length
99.2%	1333	12	11476

Matches 1344; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 TTAGATATCGTGGTATGCCAGAGTTGCATCAGGCAATGCCGATCTTGAGGAAATATATG 60

10132 TTAGATATCGTGGTATGCAAGATTGATCAGGCAATGCACATCTTGAGGAAATATG 10191

61 GGGTATGTCACCTGGTTGCTTTGTTGCATACCAAGTCACAGTTTACGTCAGTCTCTTC 120

Db 10192 GGGTATGTCACCTGGTTGCTTTGTTGCATAACAAGTCACAGTTTAAAGTCAGTCTCTTC 10251

QY	121	LAGTGGTAAAAAAGCTGAGTAATTAATTCCTGTAATGAGTGAAGACTGACCAAGGCG	180
Db	10252	AAGTGGTAAAAAAGTGAATTAATTCCTGTAATGAGTGAAGACTGACCAAGGCG	10311
QY	181	AGCTGGAATTGCTTTTACCCAAACATATTTCTTAAGTGGCTGTGATTTGATATATATAC	240
Db	10312	AGCTGGAATTGCTTTTACCCAAACATATTTCTTAAGTGGCTGTGATTTGATATATATAC	10371
QY	241	CAGCACTGACATGTACTGCACTTTATGACATCTGAGCACAGTATGTTTCAAGGAAC	300
Db	10372	CAGCACTGCAATGTACTGCACTTTATGACATCTGAGCACAGTATGTTTCAAGGAAC	10431
QY	301	ATGAGGAATATAGTGTATCATCTC-AAAGAAGGATTTGTGATTTGTTTCACTTC	359
Db	10432	ATGAGGAATATAGTGTATCATCTCMAAAGAGGATTTGTGATTTGTTTCACTTC	10491
QY	360	CAGTGGAGCAATAGCTTTTGTGACTACCGTGTGGGTTCGAAGCTGGAGATGACAG	419
Db	10492	CAGTGGAGCAATAGCTTTTGTGACTACCGTGTGGGTTCGAAGCTGGAGATGACAG	10551
QY	420	GTAATGTTGCTTTTATATGTCCACCCCTTACACAGTGGGTAGTGGGGGCTTCACAC	479
Db	10552	GTAATGTTGCTTTTATATGTCCACCCCTTACACAGTGGGTAGTGGGGGCTTCACAC	10611
QY	480	TTTTAATTCACATGATAGATTTGTGTGCTGACGCTATCAATATPAAAGATAGGT	539
Db	10612	TTTTAATTCACATGATAGATTTGTGTGCTGACGCTATCAATATPAAAGATAGGT	10671
QY	540	AATTTGTAAAGAAAAGATTTGCTCGAGCTGTGTATGCCATAGGAAGGTTGTTCTTACA	599
Db	10672	AATTTGTAAAGAAAAGATTTGCTCGAGCTGTGTATGCCATAGGAAGGTTGTTCTTACA	10731
QY	600	GGCCCCAGACATPACCATTCATCATATATATCTACTAAGTGTGTTTCATCTTAT	659
Db	10732	GGCCCCAGACATPACCATTCATCATATATATCTACTAAGTGTGTTTCATCTTAT	10791
QY	660	GCTCAGTTGAGCTCGTCTAATACTAGAATATTTTCCGAATCTACCTTACCATCTAG	719
Db	10792	GCTCAGTTGAGCTCGTCTAATACTAGAATATTTTCCGAATCTACCTTACCATCTAG	10851
QY	720	CAGTTTAAAGGACCCCATTTGGAACAATTTGGCTGGGTTTGTATGTTGACAGTTTC	779
Db	10852	CAGTTTAAAGGACCCCATTTGGAACAATTTGGCTGGGTTTGTATGTTGACAGTTTC	10911
QY	780	TGCTATTTCTTAATCAGGTGGCCTTGACTGTGACATGACACTCTTGTGTGATTCAGCA	839
Db	10912	TGCTATTTCTTAATCAGGTGGCCTTGACTGTGACATGACACTCTTGTGTGATTCAGCA	10971
QY	840	GGGTTGATCATGATGTGACTACTTACAAACCTTAAGTGTGGCTCAGAGGCTACCTGAC	899
Db	10972	GGGTTGATCATGATGTGACTACTTACAAACCTTAAGTGTGGCTCAGAGGCTACCTGAC	11031
QY	900	TGCTTTGACTCAACTGCTTACAATCTGAATCAACTTCCCAATGCTGATGCCCTTGA	959
Db	11032	TGCTTTGACTCAACTGCTTACAATCTGAATCAACTTCCCAATGCTGATGCCCTTGA	11091
QY	960	GGAAACATCCGCATGACAAACAGGCGCGCTCTTTCTCGGTGTACACTTCGAGACAACTGC	1019
Db	11092	GGAAACATCCGCATGACAAACAGGCGCGCTCTTTCTCGGTGTACACTTCGAGACAACTGC	11151
QY	1020	GGTGGTATAGCCCTTACAGAGTAAAGAACAGACAGCGGCTTGTACAAAGGCAAGAGAGA	1079
Db	11152	GGTGGTATAGCCCTTACAGAGTAAAGAACAGACAGCGGCTTGTACAAAGGCAAGAGAGA	11211
QY	1080	ACTTCAGAGAGCTGTGATCTGTAGCGAAGCGACGCGCAACGCGCGAGGCTGCTCCA	1139
Db	11212	ACTTCAGAGAGCTGTGATCTGTAGCGAAGCGACGCGCGAGGCTGCTCCA	11271
QY	1140	GGCCCATGACTGGGAGGGGATCGTGGCCTTCCCAAGATGCCAGGAGAGAGCATGATATA	1199
Db	11272	GGCCCATGACTGGGAGGGGATCGTGGCCTTCCCAAGATGCCAGGAGAGAGCATGATATA	11331

QY	1200	GCTACTCTGTTGTTAGAGCCCTGGAAGAAATA	TGACGGAGCCTGGGTCTTTGTTGTGCTGC	1259
Db	11332	GCTACTCTGTTGTTGTAAGCGCTCGAAGAATA	TGACCGGCTGGGTCTTTGTTGTGCTGC	11391
QY	1260	ACTGAAACCTCCTCCATCTTGACATCATCCG	GTGTTTGTATCATATAATAATTT	1319
Db	11332	ACTGAAACCTCCTCCATCTTGACATCATCCG	GTGTTTGTATCATATAATAATTT	11455
QY	1320	GCCCGTGCGCTCAACGTGAAAAATCC	1344	
Db	11452	GCCCGTGCGCTCAACGTGAAAAATCC	11476	

```

RESULT 2
US-10-260-238-3410
; Sequence 3410, Application US/10260238
; Publication No. US20040016025A1
;
GENERAL INFORMATION:
;
APPLICANT: Budworth, Paul R.
APPLICANT: Moushaher, Todd G.
APPLICANT: Briggs, Steven P.
APPLICANT: Cooper, Bret
APPLICANT: Glazebrook, Jane
APPLICANT: Goff, Stephen A.
APPLICANT: Katagiri, Fumiyuki
APPLICANT: Kreps, Joel
APPLICANT: Provart, Nicholas
APPLICANT: Rieke, Darrell
APPLICANT: Zhu, Tong
;
TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
FILE REFERENCE: 60111-NP
CURRENT APPLICATION NUMBER: US/10/260,238
CURRENT FILING DATE: 2002-09-25
PRIOR APPLICATION NUMBER: US 60/325,448
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR FILING DATE: 2002-04-04
;
NUMBER OF SEQ ID NOS: 6077
;
SEQ ID NO 3410
;
LENGTH: 1119
;
TYPE: DNA
;
ORGANISM: Triticum aestivum
;
US-10-260-238-3410

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Query Match      27.5%; Score 370; DB 15; Length 1119;
Best Local Similarity 100.0%; Pred. No. 3.8e-105;
Matches 370; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY	961	GAACAATCCGACATGAACAAGCCGGGCTCTTCTCGGATCACTCCGAGCAAGACTCG	1027
Db	727	GAACAATCCGACATGAACAAGCCGGGCTCTTCTCGGATCACTCCGAGCAAGACTCG	786
QY	1021	GTGCGTATATGCCCTTACAGAGTAGAACCAAGCAGCGCTTGTTACAGGCAAGAGAGA	1088
Db	787	GTGCGTATATGCCCTTACAGAGTAGAACCAAGCAGCGCTTGTTACAGGCAAGAGAGA	846
QY	1081	CTCCAGAGAGGCTCGTAGATCGGACGACGAGCGCAACGGCGCGAGGCTGCTCAAG	1144
Db	847	CTCCAGAGAGGCTCGTAGATCGGACGACGAGCGCAACGGCGCGAGGCTGCTCAAG	906
QY	1141	CGCCATGACTGGAGAGGGATGTGCTCTTCCCCAGATGCCAGAGAGACAGATGGATNG	1207
Db	907	CGCCATGACTGGAGAGGGATGTGCTCTTCCCCAGATGCCAGAGAGAGACAGATGGATNG	966
QY	1201	GTAGCTTGTTGGTGAAGCGCTCGAAAGAAATAGACGGGCTGGGTGTTGTTGTGCTGCA	1266
Db	967	GTAGCTTGTTGGTGAAGCGCTCGAAAGAAATAGACGGGCTGGGTGTTGTTGTGCTGCA	1026
QY	1261	CTGAACCTCTCTCTCTATCTTGACACTTCCCGGTGTTTTTGACATATTAACAATAATNG	1332
Db	1027	CTGAACCTCTCTCTCTATCTTGACACTTCCCGGTGTTTTTGACATATTAACAATAATNG	1088

QY 1321 CCCGTGGCCT 1330  
1087 CCCGTGGCCT 1096

## RESULT 3

US-10-434-893A-1

; Sequence 1, Application US/10434893A  
; Publication No. US2004006083A1  
; GENERAL INFORMATION:  
; APPLICANT: Ahmed Regina  
; APPLICANT: Matthew Kennedy Morell  
; APPLICANT: Sadegur Rahman  
; TITLE OF INVENTION: Barley with altered branching enzyme activity and starch and stac  
; FILE REFERENCE: 69425  
; CURRENT APPLICATION NUMBER: US/10/434,893A  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 2.1  
; SEQ ID NO 1  
; LENGTH: 2554  
; TYPE: DNA  
; ORGANISM: Hordeum vulgare  
; FEATURE:  
; OTHER INFORMATION: SSBELTA CDNA  
; US-10-434-893A-1

Query Match 19.6%; Score 263.6; DB 12; Length 2554;  
Best Local Similarity 87.5%; Pred. No. 2.2e-71;  
Matches 343; Conservative 0; Mismatches 24; Indels 25; Gaps 4;

QY 961 GAACATCCGCATGACAGACGCGCGCTCTTTCTCGGTGTACACTCCGACGAACTGCG 1020  
DB 2128 GAACATCCGCATGACAGACGCGCGCTCTTTCTCGGTGTACACTCCGACGAACTGCG 2187  
QY 1021 GTCGTGATGCCCTTACAGAGTAAGAACACAGCGCGCTTTTTCACAGCAAGAGAGAA 1080  
DB 2188 GTCGTGATGCCCTTACAGAGTAAGAACACAGCGCGCTTTTTCACAGCAAGAGAGAA 2247  
QY 1081 CTCGAGAGAGCGCTGATGCTGAGGAGAGCGAGCGGCGAGCGGCTCTCCAG 1140  
DB 2248 CTCGAGAGAGCGCTGATGCTGAGGAGAGCGAGCGGCGAGCGGCTCTCCAG 2307  
QY 1141 CGCCATGACTGGAGAGGATCGTGCCTCTTCCCAAGATCCAGAGAGAGATGATAG 1200  
DB 2308 CGCCGATGAGGAGAGGATCGTGCCTCTTCCCAAGATCTAGAGAGATGATGATAG 2367  
QY 1201 GTAGCTTGTGTAGCGCT-----CGAAGAAATGAGCGGCGCTG 1243  
DB 2368 GTAGCTTGTGTAGCGCTCGTTTCAAGTGAAGTGCAGAAAGAAATGAGCGGCGCTG 2427  
QY 1244 GTG-----TTGTGTGCTGCTGCTGAGACCGTCCGCTATCTGACATTCGCGGTGTTT 1299  
DB 2428 GTGACATTTTGTAGTGTGCTGCTGAGAC---CATCTTATCTCTCAATTCGCGGTGTTT 2484  
QY 1300 TGTACATAT-AACTATATATGCGCGCTGCGCT 1310  
DB 2485 TGTACATATAACTAATATGCGCGCTGCGCT 2516

## RESULT 4

US-09-792-127-1

; Sequence 1, Application US/09792127  
; Patent No. US0020002713A1  
; GENERAL INFORMATION:  
; APPLICANT: Allen, Steve  
; APPLICANT: Beckles, Diane M.  
; APPLICANT: Butler, Karla  
; APPLICANT: Pearlstein, Rich  
; TITLE OF INVENTION: Starch Branching Enzyme IId  
; FILE REFERENCE: BB1439 US NA

; CURRENT APPLICATION NUMBER: US/09/792,127  
; CURRENT FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: 60/186098  
; PRIOR FILING DATE: 2000-03-01  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 1  
; LENGTH: 2559  
; TYPE: DNA  
; ORGANISM: Triticum aestivum  
; US-09-792-127-1

Query Match 9.1%; Score 122.6; DB 9; Length 2559;  
Best Local Similarity 78.9%; Pred. No. 5.8e-27;  
Matches 146; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 264 TTTATGACATCTGAGACCAAGATATGTTTCAAGAAACATGAGAAAGATAGGTGATCATC 323  
DB 1776 TTTATGACATCAAGACCAAGATATCTGGAACATGAGAAAGATAGGTGATCTGTG 1835  
QY 324 CTCAAAAGAGAGATTGTTTGTATTTTTCACCTTCCACTGAGCAATAGCTTTTGTAC 383  
DB 1836 TTTGAAAAGAGGACTTGTTATTTGTCTCAACTTCCACTGAGATAGCTATTTTGCAC 1895  
QY 384 TACCGTGTGGGTGTTCCAGCGCTGGAGATGACATGATGCTTTCATTGTGTCA 443  
DB 1896 TACCGGTGTGGGTGTTTAAAGCTTGGAGATGACATGATGCTTTCATTGTGTCA 1955  
QY 444 CCCTT 448  
DB 1956 CTCTT 1960

## RESULT 5

US-09-792-127-3

; Sequence 3, Application US/09792127  
; Patent No. US20020002713A1  
; GENERAL INFORMATION:  
; APPLICANT: Allen, Steve  
; APPLICANT: Beckles, Diane M.  
; APPLICANT: Butler, Karla  
; APPLICANT: Pearlstein, Rich  
; TITLE OF INVENTION: Starch Branching Enzyme IId  
; FILE REFERENCE: BB1439 US NA  
; CURRENT APPLICATION NUMBER: US/09/792,127  
; CURRENT FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: 60/186098  
; PRIOR FILING DATE: 2000-03-01  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 3  
; LENGTH: 3039  
; TYPE: DNA  
; ORGANISM: Triticum aestivum  
; US-09-792-127-3

Query Match 9.1%; Score 122.6; DB 9; Length 3039;  
Best Local Similarity 78.9%; Pred. No. 6.5e-27;  
Matches 146; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 264 TTTATGACATCTGAGACCAAGATATGTTTCAAGAAACATGAGAAAGATAGGTGATCATC 323  
DB 2256 TTTATGACATCAAGACCAAGATATCTGGAACATGAGAAAGATAGGTGATCTGTG 2315  
QY 324 CTCAAAAGAGAGATTGTTTGTATTTTTCACCTTCCACTGAGCAATAGCTTTTGTAC 383  
DB 2316 TTTGAAAAGAGGACTTGTTATTTGTCTCAACTTCCACTGAGATAGCTATTTGTAC 2375  
QY 384 TACCGTGTGGGTGTTCCAGCGCTGGAGATGACATGATGCTTTCATTGTGTCA 443  
DB 2376 TACCGGTGTGGGTGTTTAAAGCTTGGAGATGACATGATGCTTTCATTGTGTCA 2435  
QY 444 CCCTT 448

Db 2436 CTCCTT 2440

## RESULT 6

US-10-260-238-3480  
Sequence 3480, Application US/10260238  
Publication No. US20040016025A1  
GENERAL INFORMATION:

APPLICANT: Budworth, Paul R.  
APPLICANT: Moughamer, Todd G.  
APPLICANT: Briggs, Steven P.  
APPLICANT: Cooper, Bret  
APPLICANT: Glazebrook, Jane  
APPLICANT: Goff, Stephen A.  
APPLICANT: Katagiri, Fumiyaki  
APPLICANT: Kreps, Joel  
APPLICANT: Provart, Nicholas  
APPLICANT: Rieke, Darrell

APPLICANT: Zhu, Tong  
TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION

FILE REFERENCE: 60111-NP

CURRENT APPLICATION NUMBER: US/10/260,238

CURRENT FILING DATE: 2002-09-26

PRIOR FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: US 60/325,277

PRIOR FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: US 60/370,620

PRIOR FILING DATE: 2002-04-04

NUMBER OF SEQ ID NOS: 6077

SEQ ID NO 3480

LENGTH: 1267

TYPE: DNA

ORGANISM: Triticum aestivum

US-10-260-238-3480

Query Match  
Best Local Similarity 84.1%; Score 122.4; DB 15; Length 1267;  
Pred. No. 4.1e-27;  
Matches 138; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 264 TTATGACATCTGAGCAGCATGATGTTCAACGAAACATGAGAAATAGGTATCATC 323

Db 513 TTATGACATCTGAGCAGCATGATGTTCAACGAAACATGAGAAATAGGTATCATC 572

QY 324 CTCGAAAGAGAGATTGGTATTTGTTTCACTTCCATGAGCAATAGCTTTTGGAC 383

Db 573 TTGAAAAAGGGAGCTTGATTTGTTGTTCACTTCCATGAGCAATAGCTTTTGGAC 632

QY 384 TACCGGTGGGTGTTCCAGCCTGGAGAGTACAGTATCTT 427

Db 633 TACCGGTGGGTGTTTAAAGCCTGGAGAGTACAGTATCTT 676

US-10-260-238-5563

Sequence 5563, Application US/10260238  
Publication No. US20040016025A1  
GENERAL INFORMATION:

APPLICANT: Budworth, Paul R.  
APPLICANT: Moughamer, Todd G.  
APPLICANT: Briggs, Steven P.  
APPLICANT: Cooper, Bret  
APPLICANT: Glazebrook, Jane  
APPLICANT: Goff, Stephen A.  
APPLICANT: Katagiri, Fumiyaki  
APPLICANT: Kreps, Joel  
APPLICANT: Provart, Nicholas  
APPLICANT: Rieke, Darrell

APPLICANT: Zhu, Tong

TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION

FILE REFERENCE: 60111-NP

CURRENT APPLICATION NUMBER: US/10/260,238

PRIOR FILING DATE: 2002-04-04

NUMBER OF SEQ ID NOS: 6077

SEQ ID NO 3480

LENGTH: 1267

TYPE: DNA

ORGANISM: Triticum aestivum

US-10-260-238-3480

Query Match  
Best Local Similarity 84.1%; Score 122.4; DB 15; Length 1267;  
Pred. No. 4.1e-27;  
Matches 138; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 264 TTATGACATCTGAGCAGCATGATGTTCAACGAAACATGAGAAATAGGTATCATC 323

CURRENT FILING DATE: 2002-09-26  
PRIOR APPLICATION NUMBER: US 60/325,448  
PRIOR FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: US 60/325,277  
PRIOR FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: US 60/370,620  
PRIOR FILING DATE: 2002-04-04  
NUMBER OF SEQ ID NOS: 6077  
SEQ ID NO 5563  
LENGTH: 636  
TYPE: DNA  
ORGANISM: Zea mays  
US-10-260-238-5563

Query Match  
Best Local Similarity 82.6%; Score 120.6; DB 15; Length 636;  
Pred. No. 9.2e-27;  
Matches 138; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 262 AGTTATGACATCTGAGCAGCATGATGTTTCAACGAAACATGAGAAATAGGTATCATC 321

Db 323 AATTCATGACATCTGATCAGCAGTATATTTCCGAAACATGAGAGATTAAGTATCTG 382

QY 322 TCCTCAAAAGAGAGATTGGTATTTGTTTCACTTCCATGAGCAATAGCTTTTGGAC 381

Db 383 TGTTGAAAAAGGGAGATTGGTATTTGTTTCACTTCCATGAGCAATAGCTTTTGGAC 442

QY 382 ACTACCGTGGGTGTTTCCAGCCTGGAGAGTACAGTATGCTTG 428

Db 443 ACTACCGTGGGTGTTTCCAGCCTGGAGAGTACAGTATGCTTG 489

## RESULT 8

US-10-434-893A-2  
Sequence 2, Application US/10434893A  
Publication No. US2004006083A1  
GENERAL INFORMATION:

APPLICANT: Ahmed Regina  
APPLICANT: Matchew Kennedy Morell  
TITLE OF INVENTION: Barley with altered branching enzyme activity and starch and ste  
TITLE OF INVENTION: containing products with an increased amylose content  
FILE REFERENCE: 69425  
CURRENT APPLICATION NUMBER: US/10/434,893A  
CURRENT FILING DATE: 2003-05-09  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: PatentIn version 2.1  
SEQ ID NO 2  
LENGTH: 2780  
TYPE: DNA  
ORGANISM: Hordeum vulgare  
FEATURE:  
OTHER INFORMATION: SSBEIIB cDNA  
US-10-434-893A-2

Query Match  
Best Local Similarity 84.8%; Score 119.6; DB 12; Length 2780;  
Pred. No. 5.4e-26;  
Matches 134; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 264 TTATGACATCTGAGCAGCATGATGTTTCAACGAAACATGAGAAATAGGTATCATC 323

Db 2182 TTATGACATCTGAGCAGCATGATGTTTCAACGAAACATGAGAAATAGGTATCATC 2241

QY 324 CTCGAAAGAGAGATTGGTATTTGTTTCACTTCCATGAGCAATAGCTTTTGGAC 383

Db 2242 TTGAAAAAGGGAGCTTGATTTGTTTCACTTCCATGAGCAATAGCTTTTGGAC 2301

QY 384 TACCGGTGGGTGTTTCCAGCCTGGAGAGTACAGTATCTT 421

Db 2302 TACCGGTGGGTGTTTAAAGCCTGGAGAGTACAGTATCTT 2339

US-10-260-238-1027

```
/ Sequence 1027, Application US/10260238
/ Publication No. US20040016025A1
/ GENERAL INFORMATION:
/ APPLICANT: Budworth, Paul R.
/ APPLICANT: Moughamer, Todd G.
/ APPLICANT: Briggs, Steven P.
/ APPLICANT: Cooper, Bret
/ APPLICANT: Glazebrook, Jane
/ APPLICANT: Goff, Stephen A.
/ APPLICANT: Katagiri, Fumiyaki
/ APPLICANT: Kieps, Joel
/ APPLICANT: Pevsart, Nicholas
/ APPLICANT: Rieke, Darrell
/ APPLICANT: Zhu, Tong
/ TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
/ FILE REFERENCE: 60111-NP
/ CURRENT APPLICATION NUMBER: US/10/260,238
/ CURRENT FILING DATE: 2002-09-26
/ PRIOR APPLICATION NUMBER: US 60/325,448
/ PRIOR FILING DATE: 2001-09-26
/ PRIOR APPLICATION NUMBER: US 60/325,277
/ PRIOR FILING DATE: 2001-09-26
/ PRIOR APPLICATION NUMBER: US 60/370,620
/ PRIOR FILING DATE: 2002-04-04
/ NUMBER OF SEQ ID NOS: 6077
/ SEQ ID NO 1027
/ LENGTH: 1642
/ TYPE: DNA
/ ORGANISM: Oryza sativa
/ US-10-260-238-1027

Query Match      8.0%; Score 107.2; DB 15; Length 1642;
Best Local Similarity 77.4%; Pred. No. 3e-22;
Matches 130; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 259 TGCAATTATGACATCTTGAGCACGATATGTTTCACGGAACATGAGAAATAGGTGA 318
DB 1281 TGGGGTTCATGACATCAGACACCACTGATCTCGAAAGCATGAAAGATGA 1340
QY 319 TCATCTTCAAAAGAGAGATTGGTATTTGTTTCACTTCACCTGAGCAATAGCTTT 378
DB 1341 TTATATTTGAAAGGAGATCTGGTATTTGTTCAACTTCAGAGTAAACAGCTATT 1400
QY 379 TTGACTACCGTGTGGGTGTTCCAGCCTGGGAGATGACAGGTATGCT 426
DB 1401 TTGACTACCGTGTGGGTGTTTAAAGCCAGGAAATATTAAGGTGCT 1448

RESULT 10
US-09-770-149-955/c
/ Sequence 955, Application US/09770149
/ Patent No. US20020059663A1
/ GENERAL INFORMATION:
/ APPLICANT: Gorlach, Jorn
/ APPLICANT: An, Yong-Qiang
/ APPLICANT: Hamilton, Carol M.
/ APPLICANT: Price, Jennifer L.
/ APPLICANT: Raines, Tracy M.
/ APPLICANT: Yu, Yang
/ APPLICANT: Rameaka, Joshua G.
/ APPLICANT: Page, Amy
/ APPLICANT: Matthew, Abraham V.
/ APPLICANT: Ledford, Brooke L.
/ APPLICANT: Woessner, Jeffrey P.
/ APPLICANT: Haas, William David
/ APPLICANT: Garcia, Carlos A.
/ APPLICANT: Kricker, Maja
/ APPLICANT: Slader, Ted
/ APPLICANT: Davis, Keith R.
/ APPLICANT: Allen, Keith
/ APPLICANT: Hoffman, Neil
/ APPLICANT: Hurban, Patrick
/ TITLE OF INVENTION: Expressed Sequences of Arabidopsis
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```
/ TITLE OF INVENTION: thaliana
/ FILE REFERENCE: 2024 (PARA-013PRV)
/ CURRENT APPLICATION NUMBER: US/09/770,149
/ CURRENT FILING DATE: 2001-01-26
/ PRIOR APPLICATION NUMBER: 60/178,506
/ PRIOR FILING DATE: 2000-01-27
/ NUMBER OF SEQ ID NOS: 999
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 955
/ LENGTH: 602
/ TYPE: DNA
/ ORGANISM: Arabidopsis thaliana
/ US-09-770-149-955

Query Match      7.2%; Score 97; DB 9; Length 602;
Best Local Similarity 70.3%; Pred. No. 2.4e-19;
Matches 130; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 264 TTTATGACATCTGAGCACGATATGTTTCACGGAACATGAGAAATAGGTATCATC 323
DB 490 TTTATGACTTCGAGACCAATTCATATCAAGAAAGCAGAGAGATAGATATCGTA 431
QY 324 CTCAAAAGAGAGATTGGTATTTGTTTCACTTCACCTGAGCAATAGCTTTTTCAC 383
DB 430 TTGAAAAGAGGTATCTGCTTTGTTCTTTAACTTCACTGACACGAGCTACTTGAT 371
QY 384 TACCGTGTGGGTGTTCCAGCCTGAGAGATGAGATGCTTTCATTGTCGA 443
DB 370 TACCGCATTTGTTGCTTCAGACCTCGAATAATATAGATCGATTGATCGAGACATCT 311
QY 444 CCCTT 448
DB 310 CTCCT 306

RESULT 11
US-09-938-842A-872
/ Sequence 872, Application US/09938842A
/ Patent No. US20020160378A1
/ GENERAL INFORMATION:
/ APPLICANT: Harper, Jeff
/ APPLICANT: Kieps, Joel
/ APPLICANT: Wang, Xun
/ APPLICANT: Zhu, Tong
/ TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
/ TITLE OF INVENTION: SAME, AND METHODS OF USE
/ FILE REFERENCE: SRIPI300-3
/ CURRENT APPLICATION NUMBER: US/09/938,842A
/ CURRENT FILING DATE: 2001-08-24
/ PRIOR APPLICATION NUMBER: US 60/227,866
/ PRIOR FILING DATE: 2000-08-24
/ PRIOR APPLICATION NUMBER: US 60/264,647
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/300,111
/ PRIOR FILING DATE: 2001-06-22
/ NUMBER OF SEQ ID NOS: 5379
/ SEQ ID NO 872
/ LENGTH: 2418
/ TYPE: DNA
/ ORGANISM: Arabidopsis thaliana
/ US-09-938-842A-872

Query Match      7.2%; Score 97; DB 9; Length 2418;
Best Local Similarity 70.3%; Pred. No. 6.4e-19;
Matches 130; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 264 TTTATGACATCTGAGCACGATATGTTTCACGGAACATGAGAAATAGGTATCATC 323
DB 2098 TTTATGACTTCGAGACCAATTCATATCAAGAAAGCAGAGAGATAGATATCGTA 2157
QY 324 CTCAAAAGAGAGATTGGTATTTGTTTCACTTCACCTGAGCAATAGCTTTTTCAC 383
DB 2158 TTGAAAAGAGGTATCTGCTTTGTTCTTTAACTTCACTGACACGAGCTACTTGAT 2217
```

QY 384 TACCGTGTGGTGTTCACAGCCCTGGAGATACAGGATGATGCTTTCATTGTCGA 443  
DB 2218 TACCGCATTTGTTGCTTCACAGCCCTGGAGAAATATAGATCGATTGAGCTCGGAGCATCT 2277  
QY 444 CCCTT 448  
DB 2278 CTCTT 2282

RESULT 12  
US-09-938-842A-872  
Sequence 872, Application US/09338842A  
Publication No. US2004009476A9  
GENERAL INFORMATION:  
APPLICANT: Harper, Jeff  
APPLICANT: Krepes, Joel  
APPLICANT: Wang, Xun  
APPLICANT: Zhu, Tong  
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
TITLE OF INVENTION: SAME, AND METHODS OF USE  
FILE REFERENCE: SRIPI300-3  
CURRENT APPLICATION NUMBER: US/09/938, 842A  
CURRENT FILING DATE: 2001-08-24  
PRIOR APPLICATION NUMBER: US 60/227, 866  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: US 60/264, 647  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/300, 111  
PRIOR FILING DATE: 2001-06-22  
NUMBER OF SEQ ID NOS: 5379  
SEQ ID NO 872  
LENGTH: 2418  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
US-09-938-842A-872

Query Match 7.2%; Score 97; DB 11; Length 2418;  
Best Local Similarity 70.3%; Pred. No. 6.4e-19;  
Matches 130; Conservative 0; Mismatches 55; Indels 0; Gaps 0;  
QY 264 TTATGATCATCTGAGACCAAGTATGTTTCACGAAACATGAGAGATAGGTGATCATC 323  
DB 2098 TTTATGATCTTCGAGACCAATTCATACAGAAAGAGAGAGATAGATATCGTA 2157  
QY 324 CTCAAGAGAGATTGGTATTTGTTTTCACCTTCGAGAGAAATAGCTTTTTCAC 383  
DB 2158 TTCGAAAGAGGTATCTGCTCTTTGCTTTTAACTTCACTGACGACGACTACTTGTAT 2217  
QY 384 TACCGTGTGGTGTTCACAGCCCTGGAGATACAGGATGATGCTTTCATTGTCGA 443  
DB 2218 TACCGCATTTGTTGCTTCACAGCCCTGGAGAAATATAGATCGATTGAGCTCGGAGCATCT 2277  
QY 444 CCCTT 448  
DB 2278 CTCTT 2282

RESULT 13  
US-10-056-454A-17  
Sequence 17, Application US/10056454A  
Publication No. US20030166919A1  
GENERAL INFORMATION:  
APPLICANT: National Starch and Chemical Investment Holding Corporation  
TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: National Starch and Chemical Investment Holding Corporation  
STREET: 1000 Unigema Blvd.  
CITY: Newcasttle  
STATE: Delaware  
COUNTRY: United States of America  
ZIP: 19720

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/056, 454A  
FILING DATE: 25-Jun-2002  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2529 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
US-10-056-454A-17

Query Match 7.1%; Score 95.4; DB 14; Length 2529;  
Best Local Similarity 69.0%; Pred. No. 2.1e-18;  
Matches 129; Conservative 1; Mismatches 57; Indels 0; Gaps 0;  
QY 262 AGTTATGATCATCTGAGACCAAGTATGTTTCACGAAACATGAGAGATAGGTGATCA 321  
DB 2175 AGTTATGATCTTCAGAACCACTTATCATACGAAAGATGAGAGATAGATGTTG 2234  
QY 322 TCCTCAAGAGAGATTGGTATTTGTTTTCACCTTCGAGAGCAATAGCTTTTTCG 381  
DB 2235 TATTGAABFAGAGAACTAGATTTTGTCTTTTATTTTCACTGACAAATAGCTATTCAG 2294  
QY 382 ACTACCGTGTGGTGTTCACAGCCCTGGAGAGATACAGGATGATGCTTTCATTGTC 441  
DB 2295 ACTATCGCATAGGCTGCTGAGCCCTGGAGAAATACAGGTTGCTTGACATCAGATCATC 2354  
QY 442 CACCTT 448  
DB 2355 CACTTTT 2361

RESULT 14  
US-10-056-454A-13  
Sequence 13, Application US/10056454A  
Publication No. US20030166919A1  
GENERAL INFORMATION:  
APPLICANT: National Starch and Chemical Investment Holding Corporation  
TITLE OF INVENTION: Improvements in or Relating to Plant Starch Composition  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: National Starch and Chemical Investment Holding Corporation  
STREET: 1000 Unigema Blvd.  
CITY: Newcasttle  
STATE: Delaware  
COUNTRY: United States of America  
ZIP: 19720  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/056, 454A  
FILING DATE: 25-Jun-2002  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2975 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
US-10-056-454A-13  
Query Match 6.9%; Score 92.6; DB 14; Length 2975;  
Best Local Similarity 68.4%; Pred. No. 1.8e-17;  
Matches 128; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY	262	AGTTTATGATCATCTGGACACAGATATTTTCAACGGAAACATATGAGAAATGAAAGGTATCA	321
Db	2403	AGTTTATGATCTTACGAAACACCAAGTTCAATACCAAAAGATGAAGAGATAGATGATGG	2462
QY	322	TCTCTCAAAAGAGAGATTTGATTTTTCACATTTCCACTGGACATATGCTTTTGG	381
Db	2463	TATTTGAAAGAGAAACCTAGTTTTCCTTTTATTTTCACTGGACAAATAGCATTTACG	2522
QY	382	ACTATCGCTGTTGGGTCTTCAAGCCTGGAAATCAAGATATGCTTACCTTTTCATGTC	441
Db	2523	ACTATCCCAATAGGCTGCTGCTGAAGCTGGAAAATACAAAGTTGTTCTTTGACTCAGATATC	2582
QY	442	CACGCTT	448
Db	2583	CACTTTT	2589

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RESULT 15
US-10-425-114-8329
: Sequence 8329, Application US/10425114
: Publication No. US2004003488A1
: GENERAL INFORMATION:
: APPLICANT: Liu, Jingdong
: APPLICANT: Zhou, Yihua
: APPLICANT: Kovalic, David K.
: APPLICANT: Screen, Steven E
: APPLICANT: Tabaska, Jack E
: APPLICANT: Cao, Yongwei
: TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
: FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
: FILE REFERENCE: 38-21(5313)B
: CURRENT APPLICATION NUMBER: US/10/425,114
: CURRENT FILING DATE: 2003-04-28
: NUMBER OF SEQ ID NOS: 73128
: SEQ ID NO 8329
: LENGTH: 1867
: TYPE: DNA
: ORGANISM: Glycine max
: FEATURE:
: OTHER INFORMATION: Clone ID: 700747645_FLI
US-10-425-114-8329

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Query Match	6.8%;	Score 91.6;	DB 12;	Length 1867;
Best Local Similarity	-68.3%;	Pred. No. 2.7e-17;		
Matches 127;	Conservative 0;	Mismatches 59;	Indels 0;	Gaps 0;

Qy	264	TTTNGACATGTGAGCAACGATATTTTACGSAACATGAGAAATAGGTGATCATC	323
Db	879	TTCAATGACTGCTGAGCAACCATATATTTACGGAAATGAAAGTGACAAATTAATAGTC	938
Qy	324	CTCAAAAGAGAGATTGTGTAATTGTGTTTCAACTTCCACTGAGACATAGCTTTTTCAC	383
Db	939	TTCGAAAGAGGCAACCTCATCTTTGTCTTCATTTTCATTTGGAACAAACGATATTCAGAT	998
Qy	384	TACGATGTTGGTGTTTCCAAAGCTTGGGAAGTACAGAGATGTTGCCTTTCATTTGTGCCA	443
Db	999	TACAGAGTTGCTGTTCAAACCCCTGGGAAATATAAGATGTCTTGGAATTCAGATGATGCC	1058
Qy	444	CCCTTC	449
Db	1059	TTGTTTC	1064

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Job time : 478.681 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 10, 2004, 03:15:20 ; Search time 3546.4 Seconds  
(without alignments)  
11317.033 Million cell updates/sec

Title: US-09-508-377-10\_COPY\_10120\_11463

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Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: em\_escba:\*  
2: em\_escbm:\*  
3: em\_escin:\*  
4: em\_escm:\*  
5: em\_escm:\*  
6: em\_escm:\*  
7: em\_escm:\*  
8: em\_escm:\*  
9: gb\_esc1:\*  
10: gb\_esc2:\*  
11: gb\_esc3:\*  
12: gb\_esc4:\*  
13: gb\_esc5:\*  
14: gb\_esc5:\*  
15: em\_escfun:\*  
16: em\_escm:\*  
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27: em\_escm:\*  
28: gb\_esc1:\*  
29: gb\_esc2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	464.8	34.6	724 13	BU607192 1G7 wheat
2	370	27.5	610 14	CD912768 G550.115M
3	366.8	27.3	573 13	BQ237446 TAR05016F
4	365.8	27.2	1107 14	CK210642 FGAS02246

5	361.6	26.9	447 9	AJ604482
6	361.6	26.9	622 14	CD890410
7	360.4	26.8	405 13	BQ242270
8	359.6	26.8	692 14	CD895041
9	358.4	26.7	414 12	BQ270799
10	358.4	26.7	491 12	BQ232268
11	358.4	26.7	897 14	CK153053
12	358.4	26.7	721 12	BQ273375
13	347.6	25.9	527 14	CD934115
14	347.6	25.9	532 14	CD899313
15	347.6	25.9	565 14	CD897227
16	347.6	25.9	569 12	BQ267927
17	347.6	25.9	680 14	CD901305
18	347.6	25.9	749 14	CD899779
19	345	25.7	350 6	AL810271
20	343.6	25.6	470 12	BQ237912
21	341.4	25.4	556 13	BQ238322
22	339.6	25.3	593 14	CD929440
23	338.6	25.0	651 14	CD453536
24	335	24.9	484 13	BQ237604
25	331	24.6	450 12	BQ137874
26	331	24.6	537 12	BQ276381
27	330	24.6	383 13	BQ579812
28	319.6	23.8	339 12	BQ275791
29	319	23.7	554 14	CA637960
30	310	23.1	744 14	CD929759
31	308	22.9	341 14	CA739027
32	293.6	21.8	358 13	BQ282638
33	283.4	20.1	334 12	BQ272536
34	280.4	20.9	354 12	BQ267589
35	277	20.6	456 12	BQ466312
36	263.6	19.6	479 12	BQ464040
37	263.6	19.6	547 9	AV919407
38	263.6	19.6	572 14	CB875153
39	263.6	19.6	629 13	BQ471544
40	263.6	19.6	628 12	AJ432603
41	263.6	19.6	766 12	BT948391
42	262	19.5	586 14	CB871991
43	256.6	19.1	642 10	AW982619
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## ALIGNMENTS

RESULT 1  
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LOCUS 1G7 wheat seed cDNA library Triticum aestivum cDNA, mRNA sequence.  
DEFINITION BU607192  
ACCESSION BU607192.1 GI:23270467  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Triticum aestivum (bread wheat)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticaceae; Triticum.  
REFERENCE  
1 (bases 1 to 724)  
Li, J., Wang, F., Li, Q., and Zhang, X.  
Expressed sequence tags analysis of a wheat seed cDNA library  
Unpublished (2002)  
Contact: Xiansheng Zhang  
Plant development molecular biology lab  
college of life sciences  
Shan dong agriculture university, Tai'an, Shan dong, China  
Tel: 086-0538-8241144  
Email: zhiwu@sdau.edu.cn.  
Location/Qualifiers  
FEATURES  
source 1..724  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4565"



## ORIGIN

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/clone_lib="wheat seed cDNA library"
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/clone_lib="wheat seed cDNA library"
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Query Match	34.6%	Score 464.8;	DB 13;	Length 724;
Best Local Similarity	81.1%;	Pred. No. 1.5e-125;		
Matches 618; Conservative	0;	Mismatches 52;	Indels 92;	Gaps 3

Best Local Similarity 81.1%; Pred. No. 1.5e-125;

Matches 618; Conservative 0; Mismatches 52; Indels 92; Gaps 3.

Db	581	AGGAAGGTTGTTCTTAACAGGCCCGGAGACATACCTTCAATTCATTTATCTCTAAAG	640
Db	24	AGGTCGACGGTATCGATAGACTTATATCGAATTCGCGGATTCATTTATCTACTTAAG	83
Qy	641	TGTTTGGTTTCATCTTTATGCTGACGTTGAGCTCGGTCTAATACTAGAACTATTTCCGAA	700
Db	84	GGTTTGTTACATCTTTGTACTGATTGAGCTCACTCAATACGAACTGTTTACCGAA	143
Qy	701	TCCTACCCCTAACCATCTTACAGCACTTTTAGAGAGGCCCATTTTGGACATTTGGCTGSGT	760
Db	144	TCCTACCCCTAACCATCTTACAGCACTTTTAGAGAGGCCCATTTTGGACAGTCCACTGGGTTTA	203
Qy	761	TGTTAGTTGTGACAGTTTCTGCTATTTCTTATCAGGTGCGCTTGGACTCTGACGATGCA	820
Db	204	GTTGTTGTTGTACAGCTTTCTGCTATTTCTTATCAGGTGCGCTTGGACTCTGACGATGCA	262
Qy	821	CTCTTTGGTGGATTCAAGCAGGCTTGATCATATGCTACCTACTTACACCCGTAAGTCTG	880
Db	263	CTCTTTGGTGGATTCAAGCAGGCTTGATCATATGCTACCTACTTACACAC-----	313
Qy	881	GGCTCAGAGCTTACTGCTGCTTGACTCAACTGCTTACAATCTGAACTCACTTCCC	940
Db	314	-----	313
Qy	941	AATTGCTGATCCCTTGACAGGAACATCCGCATGACACAGGCCGGGCTCTTCTCGGTT	1000
Db	314	-----GAACTCCGCATGACACAGGCCGGGCTCTTCTCGGTT	353
Qy	1001	ACACTCCGAGCAGAACTCGCGTCTGTATGTCCTTACAGAGTAAAGACACAGCGGCTT	1060
Db	354	ACACTCCGAGCAGAACTCGCGTCTGTATGTCCTTACAGAGTAAAGACACAGCGTCTT	413
Qy	1061	GTTTAAAGGCAAAAGAGAACTTCCGABAGCTCCGTGATCTGTAGCGGAAAGGACGGGCAA	1120
Db	414	GTTTAAAGGCAAAAGAGAACTTCCGABAGCTCTGTGATCTGTAGCGGAAAGGACGGGCAA	473
Qy	1121	CGGCGCAGAGCTGTCCAAAGCGCCATGACTGGGAGAGGATCGTGTCTTTGCCAGATGC	1180
Db	474	CGGCGCAGAGCTGTCTTAAAGCCCATGACTGGGAGAGGATCGTGTCTTTGCCAGATGC	533
Qy	1181	CAGAGAGCAGAGATGATAGTACTTGTGTGAGCGCTCGAAAGAAATAGACGGGCTC	1240
Db	534	CAGAGAGCAGAGATGATAGTACTTGTGTGAGCGCTCGAAAGAAATAGACGGGCTC	593
Qy	1241	TGGTGTGTTTGTGTGCTGCACTGAAACCTCTCTCTTACTTGTGACATTTCCCGTGT	1300
Db	594	TGGTGTGTTTGTGTGCTGCACT--ACCTCTCTCAATCTGTGACATTTCCCGTGT	651
Qy	1301	GTCATATTAATTAATGACCGGAGCGCTCAACGTGAAAT	1342
Db	652	GTCATATTAATTAATGACCGGAGCGCTCAACATGAAAT	653

[illegible]

## REFERENCE

AUTHOR:
TITLE:

JOURNAL

COMMENT

100

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Poolidaeae; Trilicidae; Trilicium.				
1 (bases 1 to 610)				
Genoplatane.				
Genoplatane, a major partnership french program in plant genomics				
Unpublished (2003)				
Contact: Genoplatane				
Genoplatane				
93, rue Henri Rochefort 91025 EVRY CEDEX France				
Tel: 33 1 69 47 54 00				
Fax: 33 1 69 47 54 10				
This sequence has been generated in the framework of the french				
plant genomics programme 'Genoplatane' ( <a href="http://www.genoplatane.com">http://www.genoplatane.com</a>				
and <a href="http://genoplatane-info.infobios.fr">http://genoplatane-info.infobios.fr</a> ).				

FEATURES  
source

**Source**

ORIGIN

Query Match	27.5%	Score 370	DB 14	Length 610
Best Local Similarity	100.0%	Pred. No. 1.4e-97		
Matches 370	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Matches	370;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
---------	------	--------------	----	------------	----	--------	----	------	----

961 GAACATCCGATGACACAGGCCGCTCTTTCTCGGTGTACTCCGAGCAGAACTGCG 1020

QY	961	GAACATCCGCATGACCAACAGGCCGGGCTCTTCTCGGTACACTCCGAGCAGAACTCG	1020
Db	421	GAACATCCGCATGACCAACAGGCCGGGCTCTTCTCGGTACACTCCGAGCAGAACTCG	362
QY	1021	GTCTGTATGACCTCTTACAGACTAAGAACCAACAGCGGCTGTGTACACGCAAAAGAGAA	1088
Db	361	GTCTGTATGACCTCTTACAGACTAAGAACCAACAGCGGCTGTGTACACGCAAAAGAGAA	302
QY	1081	CTCCAGAGAGCTCGTGATCGGTAGCCAGAGGACGGGCAACGGCGCGAGGCTGCTCCAAAG	1144
Db	301	CTCCAGAGAGCTCGTGATCGGTAGCCAGAGGACGGGCAACGGCGCGAGGCTGCTCCAAAG	242
QY	1141	CGCCATGACTGGAGGGGATCGTGCTTTCCCCAGATGCAGAGAGGACAGATGATAG	1200
Db	241	CGCCATGACTGGAGGGGATCGTGCTTTCCCCAGATGCAGAGAGGACAGATGATAG	182
QY	1201	GTAGCTTGTGTGAGCGCTCGAAAGAAATGAGACGGGCTGTGGTGTGTGTGCTGCA	126
Db	181	GTAGCTTGTGTGAGCGCTCGAAAGAAATGAGACGGGCTGTGGTGTGTGTGCTGCA	122
QY	1261	CTGAACCTCTCTCTATCTTGGACATTTCCCGGTGTGTTTTGTACATATTAATAATTG	132
Db	121	CTGAACCTCTCTCTATCTTGGACATTTCCCGGTGTGTTTTGTACATATTAATAATTG	62
QY	1321	CCCGTGGCT 1330	
Db	61	CCCGTGGCT 52	

RESULT 3	BQ237446/c	573 bp	mRNA	linear	EST 03-MAY-2001
LOCUS	TAB05016F12F	TAB05	Triticum aestivum	CDNA	clone TAB05016F12F, mRNA
DEFINITION	sequence.				
ACCESSION	BQ237446				
VERSION	BQ237446				
KEYWORDS	BQ237446.1	GI:20433322			
SOURCE	EST				
ORGANISM	Triticum aestivum (bread wheat)				
	Triticum aestivum				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;				
	Pooideae; Triticeae; Triticum.				
REFERENCE	1 (bases 1 to 573)				
AUTHORS	Cloutier,S.				

## AUTHORS

TITLE  
JOURNAL  
COMMENT  
Wheat functional genomics - Glenlea developing seeds cDNA libraries  
Unpublished (2002)  
Contact: Dr. Sylvie Cloutier  
Cereal Research Centre, Agriculture and Agri-food Canada  
195 Datoe Rd, Winnipeg, MB, Canada R3T 2M9  
Tel: (204) 983-2340  
Fax: (204) 983-4604  
Email: scloutier@agr.gc.ca  
was cloned directionally, not all sequences generated with reverse  
primer were from the 5' end (same with forward primer and 3' end).  
Average insert size is >2.0 kb  
Plate: 016 row: F column: 12  
Seq primer: M13 Forward.  
Location/Qualifiers  
1. 573  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/cultivar="Glenlea"  
/db\_xref="taxon:4565"  
/clone="TAE05016F12F"  
/tissue\_type="developing seeds"  
/dev\_stage="5 days after anthesis"  
/lab\_host="E. coli DH10B"  
/clone\_lib="TAE05"  
/note="Vector: pSPORT-P (Invitrogen Technologies); Site\_1:  
NotI; Site\_2: MluI; mRNA obtained from wheat seeds of  
cultivar Glenlea 5 days post-anthesis"

FEATURES  
source  
Query Match 27.3%; Score 366.8; DB 13; Length 573;  
Best Local Similarity 99.5%; Pred. No. 1.2e-96;  
Matches 366; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Db 961 GAACATCCGATGACACAGAGCCGCTCTTTCTCGGTGTAACCTCCAGCAACTGCG 1020  
413 GAACATCCGATGACACAGAGCCGCTCTTTCTCGGTGTAACCTCCAGCAACTGCG 354  
Qy 1021 GTCGTGATGCCCTTACAGAGTAAGAACAGAGGCGCTTTTACAGGCAAGAGAGAA 1080  
Db 353 GTCGTGATGCCCTTACAGAGTAAGAACAGAGGCGCTTTTACAGGCAAGAGAGAA 294  
Qy 1081 CTCAGAGAGCTCGTGAATCGTAGCGAAGCAAGCGGCGCAAGCGGCTGCTCCAA 1140  
Db 293 CTCAGAGAGCTCGTGAATCGTAGCGAAGCAAGCGGCGCAAGCGGCTGCTCCAA 234  
Qy 1141 CGCCATGACTGGAGAGGAGATCGTCTCTTCCCCAGATCCAGAGAGAGAGATGATG 1200  
Db 233 CGCCATGACTGGAGAGGAGATCGTCTCTTCCCCAGATCCAGAGAGAGAGATGATG 174  
Qy 1201 GTACTTGTGTGTGAGCCCTCGAAGAAATGAGAGCGGCGCTTTGTGTGTGTGCA 1260  
Db 173 GTAGCTTGTGTGTGAGCCCTCGAAGAAATGAGAGCGGCGCTTTGTGTGTGTGCA 114  
Qy 1261 CTGAACCTCTCCCTATCTTGACATTTCCCGTGTGTGTGTGTATATATATATG 1320  
Db 113 CTGAACCTCTCCCTATTTTGACATTTCCCGTGTGTGTGTGTATATATATATG 54  
Qy 1321 CCCGTGCGCT 1330  
Db 53 CCCGTGCGCT 44

RESULT 4  
LOCUS CK210642 1107 bp mRNA linear EST 08-DEC-2003  
DEFINITION FGAS022466 Triticum aestivum FGAS: Library 5 GATE 7 Triticum  
aestivum cDNA, mRNA sequence.  
ACCESSION CK210642.1 GI:39573032  
VERSION  
KEYWORDS EST  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Triticum.  
1 (bases 1 to 1107)  
Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D.,  
Genewein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,  
Lemieux, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilsson, D.,  
Penniket, C., Roach, J.L. and Sarhan, F.  
Functional Genomics of Abiotic Stress in Wheat and Canola Crops  
Unpublished (2003)  
Contact: Wm L Crosby  
Bioinformatics  
University of Saskatchewan, Department of Computer Science  
1C101 Engineering Building, 57 Campus Drive, Saskatoon,  
Saskatchewan, S7N 5A9, Canada  
Tel: 306 966 1769  
Fax: 306 966 2033  
Email: fgas\_estes@cs.usask.ca  
This sequence is the direct result of the Base calling software  
this sequence is the direct result of the Base calling software  
Phred (default parameters). It is the raw base calls. To aid in the  
identification of the high quality insert the software Lucy  
(default parameters) has been run on this sequence. Lucy identified  
the region [18,830].  
Plate: USB023 row: I column: 05.  
Location/Qualifiers  
1. 1107  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4565"  
/clone\_lib="Triticum aestivum FGAS: Library 5 GATE 7"  
/note="Vector: pCMV.SPORT6; Crown and developmental stages  
of spike formation in wheat cultivar Norstar. 4 mRNA  
populations were combined before constructing the library.  
The first mRNA population is from 1cm crown sections after  
30 days of cold acclimation. The second is from 1cm crown  
sections after 11 days of deacclimation (before  
deacclimation plants were fully vernalized for 49 days).  
The third is from different developmental stages of spike  
formation (5 to 50mm) that still have not emerged from the  
leaf (dissection required). The last is from different  
developmental stages of spike and seed formation after  
having emerged from the leaf (visible). First strand  
synthesis in this library was done in the presence of  
methylated dCTP thereby protecting from internal cleavage  
with NotI."

FEATURES  
source  
Query Match 27.2%; Score 365.8; DB 14; Length 1107;  
Best Local Similarity 99.2%; Pred. No. 3e-96;  
Matches 367; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Db 961 GAACATCCGATGACACAGAGCCGCTCTTTCTCGGTGTAACCTCCAGCAACTGCG 1020  
477 GAACATCCGATGACACAGAGCCGCTCTTTCTCGGTGTAACCTCCAGCAACTGCG 536  
Qy 1021 GTCGTGATGCCCTTACAGAGTAAGAACAGAGGCGCTTTTACAGGCAAGAGAGAA 1080  
Db 537 GTCGTGATGCCCTTACAGAGTAAGAACAGAGGCGCTTTTACAGGCAAGAGAGAA 596  
Qy 1081 CTCAGAGAGCTCGTGAATCGTAGCGAAGCAAGCGGCGCAAGCGGCTGCTCCAA 1140  
Db 597 CTCAGAGAGCTCGTGAATCGTAGCGAAGCAAGCGGCGCAAGCGGCTGCTCCAA 656  
Qy 1141 CGCCATGACTGGAGAGGAGATCGTCTCTTCCCCAGATCCAGAGAGAGAGATGATG 1200  
Db 657 CGCCATGACTGGAGAGGAGATCGTCTCTTCCCCAGATCCAGAGAGAGAGATGATG 716  
Qy 1201 GTAGCTTGTGTGTGAGCCCTCGAAGAAATGAGAGCGGCGCTTTGTGTGTGTGCA 1260  
Db 717 GTAGCTTGTGTGTGAGCCCTCGAAGAAATGAGAGCGGCGCTTTGTGTGTGTGCA 776  
Qy 1261 CTGAACCTCTCTATCTTGACATTTCCCGTGTGTGTGTGTATATATATATG 1320  
Db 777 CTGAACCTCTCTATCTTGACATTTCCCGTGTGTGTGTGTATATATATATG 836

ORIGIN  
Query Match 27.2%; Score 365.8; DB 14; Length 1107;  
Best Local Similarity 99.2%; Pred. No. 3e-96;  
Matches 367; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Db 961 GAACATCCGATGACACAGAGCCGCTCTTTCTCGGTGTAACCTCCAGCAACTGCG 1020  
477 GAACATCCGATGACACAGAGCCGCTCTTTCTCGGTGTAACCTCCAGCAACTGCG 536  
Qy 1021 GTCGTGATGCCCTTACAGAGTAAGAACAGAGGCGCTTTTACAGGCAAGAGAGAA 1080  
Db 537 GTCGTGATGCCCTTACAGAGTAAGAACAGAGGCGCTTTTACAGGCAAGAGAGAA 596  
Qy 1081 CTCAGAGAGCTCGTGAATCGTAGCGAAGCAAGCGGCGCAAGCGGCTGCTCCAA 1140  
Db 597 CTCAGAGAGCTCGTGAATCGTAGCGAAGCAAGCGGCGCAAGCGGCTGCTCCAA 656  
Qy 1141 CGCCATGACTGGAGAGGAGATCGTCTCTTCCCCAGATCCAGAGAGAGAGATGATG 1200  
Db 657 CGCCATGACTGGAGAGGAGATCGTCTCTTCCCCAGATCCAGAGAGAGAGATGATG 716  
Qy 1201 GTAGCTTGTGTGTGAGCCCTCGAAGAAATGAGAGCGGCGCTTTGTGTGTGTGCA 1260  
Db 717 GTAGCTTGTGTGTGAGCCCTCGAAGAAATGAGAGCGGCGCTTTGTGTGTGTGCA 776  
Qy 1261 CTGAACCTCTCTATCTTGACATTTCCCGTGTGTGTGTGTATATATATATG 1320  
Db 777 CTGAACCTCTCTATCTTGACATTTCCCGTGTGTGTGTGTATATATATATG 836

QY 1321 CCGGTGGCGCT 1330  
Db 837 CCGGTGGCGCT 846

RESULT 5  
AJ604482  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AJ604482 447 bp mRNA linear EST 03-NOV-2003  
AJ604482 T07 Triticum aestivum cDNA clone H12\_T07\_plate\_9, mRNA  
sequence.  
AJ604482.1 GI:38153674  
EST.  
Triticum aestivum (bread wheat)  
Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticaceae; Triticum.  
1 (bases 1 to 447)  
Zhang, D., Kluweva, N., Barker, G.L.A., Wilson, I.D., Edwards, K.J.,  
Close, T.J., Zheng, H., McCarter, K., Soares, B.M., and Nguyen, H.T.  
Combining expressed-sequence-tags sequencing and subtractive  
hybridization for rapid identification of differentially expressed  
genes under heat stress in wheat (Triticum aestivum (L.) Moench)  
Unpublished (2003)  
Contact: Barker GL  
University of Bristol  
Biological Sciences  
Woodland Road Bristol, BS8 1UG, United Kingdom.  
Location/Qualifiers  
1..447  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/cultivar="Mustang"  
/db\_xref="taxon:4565"  
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ORIGIN  
Query Match 26.9%; Score 361.6; DB 9; Length 447;  
Best Local Similarity 98.4%; Pred. No. 3,7e-95;  
Matches 376; Conservative 0; Mismatches 4; Indels 2; Gaps 1;

QY 961 GAACATCCGATGACAAACAGAGCGCGCTCTTCTCGGTGATCACTCCGAGCAAGTGGC 1020  
Db 63 GAACATCCGATGACAAACAGAGCGCGCTCTTCTCGGTGATCACTCCGAGCAAGTGGC 122  
QY 1021 GTGCTGTATGCCCTTACAGAGTAAGAACAGAGCGCGCTTGTACAGCAAGAGAGAA 1080  
Db 123 GTGCTGTATGCCCTTACAGAGTAAGAACAGAGCACTGCTGTACAGCAAGAGAGAA 182  
QY 1081 CTCCAGAGAGCTGTGATGCTGAGCGAAGGAGAGCGGGAACGGCGGAGGCTGCCAAG 1140  
Db 183 CTCCAGAGAGCTGTGATGCTGAGCGAAGGAGAGCGGGAACGGCGGAGGCTGCCAAG 242  
QY 1141 CGGCATGACTGGAGAGGAGATCGTGCCTTCTCCAGATGCCAGAGAGAGATGATAG 1200  
Db 243 CGGCATGACTGGAGAGGAGATCGTGCCTTCTCCAGATGCCAGAGAGAGATGATAG 302  
QY 1201 GTAGCTTGTGTGAGCGCTGAAAAGAAATGACGGGCTGGGTGTTGTGTGCTGCA 1260  
Db 303 GTAGCTTGTGTGAGCGCTGAAAAGAAATGACGGGCTGGGTGTTGTGTGCTGCTCA 362  
QY 1261 CTGAACCTCTCTCTATCTTGACATTCGCCGTTGTTTGTACATATACTAATAATTG 1320  
Db 363 CT--ACCTCTCTCTATCTTGACATTCGCCGTTGTTTGTACATATACTAATAATTG 420  
QY 1321 CCGGTGGCGCTCAAGTGAAT 1342  
Db 421 CCGGTGGCGCTCAAGTGAAT 442

RESULT 6  
CD890410/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

CD890410 622 bp mRNA linear EST 14-JUL-2003  
G118.11406R010926 G118 Triticum aestivum cDNA clone G11811406,  
mRNA sequence.  
CD890410.1 GI:32659747  
EST.  
Triticum aestivum (bread wheat)  
Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticaceae; Triticum.  
1 (bases 1 to 622)  
Genoplane.  
Genoplane, a major partnership french program in plant genomics  
Unpublished (2003)  
Contact: Genoplane

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Genoplane  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplane' (<http://www.genoplane.com>  
and <http://genoplane-info.infobiogen.fr>).  
Location/Qualifiers  
1..622  
/organism="Triticum aestivum"  
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/db\_xref="taxon:4565"  
/clone="G11811406"  
/tissue\_type="Grain (118 degrees per day after  
pollination)"  
/clone\_11b="G118"

ORIGIN  
Query Match 26.9%; Score 361.6; DB 14; Length 622;  
Best Local Similarity 98.4%; Pred. No. 4.2e-95;  
Matches 376; Conservative 0; Mismatches 4; Indels 2; Gaps 1;

QY 961 GAACATCCGATGACAAACAGAGCGCGCTCTTCTCGGTGATCACTCCGAGCAAGTGGC 1020  
Db 402 GAACATCCGATGACAAACAGAGCGCGCTCTTCTCGGTGATCACTCCGAGCAAGTGGC 343  
QY 1021 GTGCTGTATGCCCTTACAGAGTAAGAACAGAGCGCGCTTGTACAGCAAGAGAGAA 1080  
Db 342 GTGCTGTATGCCCTTACAGAGTAAGAACAGAGCACTGCTGTACAGCAAGAGAGAA 283  
QY 1081 CTCCAGAGAGCTGTGATGCTGAGCGAAGGAGAGCGGGAACGGCGGAGGCTGCCAAG 1140  
Db 282 CTCCAGAGAGCTGTGATGCTGAGCGAAGGAGAGCGGGAACGGCGGAGGCTGCCAAG 223  
QY 1141 CGGCATGACTGGAGAGGAGATCGTGCCTTCTCCAGATGCCAGAGAGAGATGATAG 1200  
Db 222 CGGCATGACTGGAGAGGAGATCGTGCCTTCTCCAGATGCCAGAGAGAGATGATAG 163  
QY 1201 GTAGCTTGTGTGAGCGCTGAAAAGAAATGACGGGCTGGGTGTTTGTACATATACTAATAATTG 1320  
Db 162 GTAGCTTGTGTGAGCGCTGAAAAGAAATGACGGGCTGGGTGTTTGTACATATACTAATAATTG 103  
QY 1261 CTGAACCTCTCTCTATCTTGACATTCGCCGTTGTTTGTACATATACTAATAATTG 1320  
Db 102 CT--ACCTCTCTCTATCTTGACATTCGCCGTTGTTTGTACATATACTAATAATTG 45  
QY 1321 CCGGTGGCGCTCAAGTGAAT 1342  
Db 44 CCGGTGGCGCTCAAGTGAAT 23

BO242270/c 405 bp mRNA linear EST 03-MAY-2002  
LOCUS TA815032A02F  
DEFINITION sequence.  
ACCESSION BO242270.1 GI:20438146  
VERSION BO242270.1  
KEYWORDS EST.  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum  
Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Triticum.  
1 (bases 1 to 405)  
REFERENCE  
AUTHORS Cloutier, S.  
TITLE Wheat functional genomics - Glenlea developing seeds cDNA libraries  
JOURNAL Unpublished (2002)  
COMMENT Contact: Dr. Sylvie Cloutier  
Cereals Research Centre, Agriculture and Agri-food Canada  
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9  
Tel: (204) 983-2340  
Fax: (204) 983-4604  
Email: scloutier@agr.gc.ca  
was cloned directionally, not all sequences generated with reverse  
primer were from the 5' end (same with forward primer and 3' end).  
Average insert size is >1.4 kb  
Plate: 032 row: A column: 02  
Seq primer: M13 Forward.  
location/Qualifiers  
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/clone="TA815032A02F"  
/tissue\_type="developing seeds"  
/dev\_stage="15 days after anthesis"  
/lab\_host="E. coli DH10B"  
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/note="Vector: PCMV-SPORE6.0 (Invitrogen Technologies);  
Site 1: NciI; Site 2: MuiI; mRNA obtained from wheat seeds  
of cultivar Glenlea 15 days post-anthesis"  
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Query Match 26.8%; Score 360.4; DB 13; Length 405;  
Best Local Similarity 98.4%; Pred. No. 8.1e-95;  
Matches 364; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 961 GAACATCCGCATGACAAAGCCGCGCTTTCTCGGTGACACTCCGAGCAAACTGCG 1020  
DB 394 GAACATCCGCATGACAAAGCCGCGCTTTCTCGGTGACACTCCGAGCAAACTGCG 335  
QY 1021 GTCGTGATGCCCCCTTACAGAGTAAGAACAGAGCGGCTTTTACAGCAAGCAAGAGAA 1080  
DB 334 GTCGTGATGCCCCCTTACAGAGTAAGAACAGAGCGGCTTTTACAGCAAGCAAGAGAA 275  
QY 1081 CTCAGAGAGCTCTGTATCTGTAGCGAAGCAAGCGGCAACGCGCGAGGCTGCTCCAG 1140  
DB 274 CTCAGAGAGCTCTGTATCTGTAGCGAAGCAAGCGGCAACGCGCGAGGCTGCTCCAG 215  
QY 1141 CGCCATGACTGGGAGGGATGCTGCTCTTCCCAATATGCCAGAGAGACAGATGAGATG 1200  
DB 214 CGCCATGACTGGGAGGGATGCTGCTCTTCCCAATATGCCAGAGAGACAGATGAGATG 155  
QY 1201 GTAGCTTGTGGTGGAGCGCTCGAAGAAATGAGACGGGCTGGGCTTTGTTGTGCTGCA 1260  
DB 154 GTAGCTTGTGGTGGAGCGCTCGAAGAAATGAGACGGGCTGGGCTTTGTTGTGCTGCA 95  
QY 1261 CTGAACCTCTCTCTATCTTGACATCTCCGGTGTGTTTGTACATATACTAATATTG 1320  
DB 94 CTGAACCTCTCTCTATCTTGACATCTCCGGTGTGTTTGTACATATACTAATATTG 35  
QY 1321 CCGGTGGCGCT 1330  
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DB 34 CCGGTGGCGTT 25  
RESULT 8  
CD895041  
LOCUS G118.127M24F010824 G118  
DEFINITION mRNA sequence.  
ACCESSION CD895041 GI:32667199  
VERSION CD895041  
KEYWORDS EST.  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum  
Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Triticum.  
1 (bases 1 to 692)  
REFERENCE  
AUTHORS Genoplatne.  
TITLE Genoplatne, a major partnership french program in plant genomics  
JOURNAL Unpublished (2003)  
COMMENT Contact: Genoplatne  
Genoplatne  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplatne' (<http://www.genoplatne.com>  
and <http://genoplatne-info.infobiogen.fr>).  
location/Qualifiers  
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/organism="Triticum aestivum"  
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pollination)"  
/clone\_id="G118"  
ORIGIN  
Query Match 26.8%; Score 359.6; DB 14; Length 692;  
Best Local Similarity 97.9%; Pred. No. 1.7e-94;  
Matches 374; Conservative 0; Mismatches 6; Indels 2; Gaps 1;  
QY 961 GAACATCCGCATGACAAAGCCGCGCTTTCTCGGTGACACTCCGAGCAAACTGCG 1020  
DB 291 GAACATCCGCATGACAAAGCCGCGCTTTCTCGGTGACACTCCGAGCAAACTGCG 350  
QY 1021 GTCGTGATGCCCCCTTACAGAGTAAGAACAGAGCGGCTTTTACAGCAAGCAAGAGAA 1080  
DB 351 GTCGTGATGCCCCCTTACAGAGTAAGAACAGAGCGGCTTTTACAGCAAGCAAGAGAA 410  
QY 1081 CTCAGAGAGCTCTGTATCTGTAGCGAAGCAAGCGGCAACGCGCGAGGCTGCTCCAG 1140  
DB 411 CTCAGAGAGCTCTGTATCTGTAGCGAAGCAAGCGGCAACGCGCGAGGCTGCTCCAG 470  
QY 1141 CGCCATGACTGGGAGGGATGCTGCTCTTCCCAATATGCCAGAGAGACAGATGAGATG 1200  
DB 471 CGCCATGACTGGGAGGGATGCTGCTCTTCCCAATATGCCAGAGAGACAGATGAGATG 530  
QY 1201 GTAGCTTGTGGTGGAGCGCTCGAAGAAATGAGACGGGCTGGGCTTTGTTGTGCTGCA 1260  
DB 531 GTAGCTTGTGGTGGAGCGCTCGAAGAAATGAGACGGGCTGGGCTTTGTTGTGCTGCA 590  
QY 1261 CTGAACCTCTCTCTATCTTGACATCTCCGGTGTGTTTGTACATATACTAATATTG 1320  
DB 591 CT--ACCTCTCTCTATCTTGACATCTCCGGTGTGTTTGTACATATACTAATATTG 648  
QY 1321 CCGGTGGCGCTCAACGTGAAT 1342  
DB 649 CCGGTGGCGCTCAACGTGAAT 670  
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RESULT 9  
LOCUS BU270799 414 bp mRNA linear EST 09-APR-2002  
DEFINITION BU270799 Y. Ogihara unpublished cDNA library, wh\_ch Triticum  
aestivum cDNA clone wh09sk12 5', mRNA sequence.  
ACCESSION BU270799  
VERSION BU270799.1 GI:20096467  
KEYWORDS EST  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Triticum.  
1 (bases 1 to 414)  
Ogihara, Y. and Murai, K.  
Expressed genes in Triticum aestivum  
Unpublished (2002)  
Contact: Tadasu Shin-i  
Center For Genetic Resource Information  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: tshini@genes.nig.ac.jp.  
Location/Qualifiers  
1..414  
/organism="Triticum aestivum"  
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Best Local Similarity 97.9%; Pred. No. 3.2e-94;  
Matches 374; Conservative 0; Mismatches 6; Indels 2; Gaps 1;  
QY 961 GAACATCCGATGACACAGGCGCGCTCTTTCTCGGTGACACTCCGAGCAAGTCCG 1020  
DB 3 GAACATCCGATGACACAGGCGCGCTCTTTCTCGGTGACACTCCGAGCAAGTCCG 62  
QY 1021 GTGCTGTATGCCCTTACAGAGTAAGAACCGACAGCGGCTTTTACAGAGGCAAGAGAGA 1080  
DB 63 GTGCTGTATGCCCTTACAGAGTAAGAACCGACAGCGGCTTTTACAGAGGCAAGAGAGA 122  
QY 1081 CTCACAGAGACTGCTGTGATGCTGAGCGAAGGAGGAGCGGCGAGGCTGCCAAG 1140  
DB 123 CTCACAGAGACTGCTGTGATGCTGAGCGAAGGAGGAGCGGCGAGGCTGCCAAG 182  
QY 1141 CGCCATGACTGGAGGAGGATGCTGCTCTTCCAGATGCCAGAGAGAGAGATGATG 1200  
DB 183 CGCCATGACTGGAGGAGGATGCTGCTCTTCCAGATGCCAGAGAGAGAGATGATG 242  
QY 1201 GTAGCTTGTGTGAGCGCTCGAAGAAATGAGCGGCGCTGGGGGTGTGCTGCA 1260  
DB 243 GTAGCTTGTGTGAGCGCTCGAAGAAATGAGCGGCGCTGGGGGTGTGCTGCA 302  
QY 1261 CTGAACCTCTCTTACTTTCACATTCGCGGTGTTTTGTACATATACTAATAATTG 1320  
DB 303 CT--ACCTCTCTCAATCTTCAATTCGCGGTGTTTTGTACATATACTAATAATTG 360  
QY 1321 CCCGTGCGCTCAACGTGAATAAT 1342  
DB 361 CCCGTGCGCTCAACGTGAATAAT 382  
RESULT 10  
LOCUS BU232268 491 bp mRNA linear EST 05-APR-2002  
DEFINITION BU232268 Y. Ogihara unpublished cDNA library, wh\_e Triticum

ACCESSION BU232268  
VERSION BU232268.1 GI:20050073  
KEYWORDS EST  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Triticum.  
1 (bases 1 to 491)  
Ogihara, Y. and Murai, K.  
Expressed genes in Triticum aestivum  
Unpublished (2002)  
Contact: Tadasu Shin-i  
Center For Genetic Resource Information  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: tshini@genes.nig.ac.jp.  
Location/Qualifiers  
1..491  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/cultivar="Chinese Spring"  
/db\_xref="taxon:4565"  
/clone="wh01m24"  
/tissue\_type="seed DPA10"  
/dev\_stage="Feekes' scale 11.2"  
/clone\_lib="Y. Ogihara unpublished cDNA library, wh\_e"  
ORIGIN  
Query Match 26.7%; Score 358.4; DB 12; Length 491;  
Best Local Similarity 97.9%; Pred. No. 3.4e-94;  
Matches 374; Conservative 0; Mismatches 6; Indels 2; Gaps 1;  
QY 961 GAACATCCGATGACACAGGCGCGCTCTTTCTCGGTGACACTCCGAGCAAGTCCG 1020  
DB 88 GAACATCCGATGACACAGGCGCGCTCTTTCTCGGTGACACTCCGAGCAAGTCCG 147  
QY 1021 GTGCTGTATGCCCTTACAGAGTAAGAACCGACAGCGGCTTTTACAGAGGCAAGAGAGA 1080  
DB 148 GTGCTGTATGCCCTTACAGAGTAAGAACCGACAGCGGCTTTTACAGAGGCAAGAGAGA 207  
QY 1081 CTCACAGAGACTGCTGTGATGCTGAGCGAAGCGAGCAACGCGAGGCTGCCAAG 1140  
DB 208 CTCACAGAGACTGCTGTGATGCTGAGCGAAGCGAGCAACGCGAGGCTGCCAAG 267  
QY 1141 CGCCATGACTGGAGGAGGATGCTGCTCTTCCAGATGCCAGAGAGAGAGATGATG 1200  
DB 268 CGCCATGACTGGAGGAGGATGCTGCTCTTCCAGATGCCAGAGAGAGAGATGATG 327  
QY 1201 GTAGCTTGTGTGAGCGCTCGAAGAAATGAGCGGCGCTGGGGGTGTGCTGCA 1260  
DB 328 GTAGCTTGTGTGAGCGCTCGAAGAAATGAGCGGCGCTGGGGGTGTGCTGCA 387  
QY 1261 CTGAACCTCTCTTACTTTCACATTCGCGGTGTTTTGTACATATACTAATAATTG 1320  
DB 388 CT--ACCTCTCTCAATCTTTCACATTCGCGGTGTTTTGTACATATACTAATAATTG 445  
QY 1321 CCCGTGCGCTCAACGTGAATAAT 1342  
DB 446 CCCGTGCGCTCAACGTGAATAAT 467  
RESULT 11  
LOCUS CK153053 897 bp mRNA linear EST 05-DEC-2003  
DEFINITION FGAS031606 Triticum aestivum FGAS: Tact2 Triticum aestivum cDNA,  
mRNA sequence.  
ACCESSION CK153053  
VERSION CK153053.1 GI:38972724  
KEYWORDS EST.

SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum  
REFERENCE Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Poideae; Triticeae; Triticum.  
1 (bases 1 to 897)  
AUTHORS Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D.,  
Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,  
Lanks, M.G., McCarthy, E.L., Monroy, A., Murak, I., Nilsson, D.,  
Penikese, C., Roach, V.L. and Sarhan, A.  
Functional Genomics of Abiotic Stress in Wheat and Canola Crops  
Unpublished (2003)  
COMMENT Contact: Mm L Crosby  
Bioinformatics  
University of Saskatchewan, Department of Computer Science  
1C101 Engineering Building, 57 Campus Drive, Saskatoon,  
Saskatchewan, S7N 5A9, Canada  
Tel: 306 966 1769  
Fax: 306 966 2033  
Email: fgas.ests@cs.usask.ca  
This sequence is the direct result of the Base calling software  
phred (default parameters). It is the raw base calls. To aid in the  
identification of the high quality insert the software Lucy  
(default parameters) has been run on this sequence. Lucy identified  
the region [125,627].  
Plate: Talt237 row: A column: 20.  
Location/Qualifiers  
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/lab\_host="DH5 alpha"  
/clone\_lib="Triticum aestivum FGAS: Talt2"  
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C114106 cold hardened at 2 C for 1 day (24 H) (tester) and  
subtracted against genotype Norstar cold hardened at 2 C  
for 21 days and 49 days (equal amount of cDNA pooled  
together before subtraction, driver). Nitro-pyrole  
anchored oligo-dT priming and non-directional cloning."

ORIGIN  
Query Match 26.7%; Score 358.4; DB 14; Length 897;  
Best Local Similarity 97.9%; Pred. No. 4,3e-94;  
Matches 374; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

QY 961 GAACATCGCATGACAGAGCGCGCTTTCTCGGTATACCTCCAGCAGACTGCG 1020  
DB 540 GAACATCGCATGACAGAGCGCGCTTTCTCGGTATACCTCCAGCAGACTGCG 481

QY 1021 GTCGTGTATGCCCTTACAGAGTAAGAACAGAGCGGCTTTGTTACAGGCAAGAGAGAA 1080  
DB 480 GTCGTGTATGCCCTTACAGAGTAAGAACAGAGCGGCTTTGTTACAGGCAAGAGAGAA 421

QY 1081 CTCAGAGAGCTCGGTATCGGTAGAGGAAGAGAGCGGCGGAGAGCTGCTCAAG 1140  
DB 420 CTCAGAGAGCTCGGTATCGGTAGAGGAAGAGAGCGGCGGAGAGCTGCTCAAG 361

QY 1141 CGCCATGACTGGAGAGGAGTCTGCTCTTCCAGATCCAGAGAGAGAGATGATAG 1200  
DB 360 CGCCATGACTGGAGAGGAGTCTGCTCTTCCAGATCCAGAGAGAGAGATGATAG 301

QY 1201 GTAGCTTGTGGTGGCGCTCGAAGAAATGAGAGGCGCTGGGTTTGTGTGCTGCA 1260  
DB 300 GTAGCTTGTGGTGGCGCTCGAAGAAATGAGAGGCGCTGGGTTTGTGTGCTGCA 241

QY 1261 CTGAACCTCTCTCTATCTTGACATTCGCGGTGTTTGTATACATATATATATG 1320  
DB 240 CT--ACCTCTCTCTATCTTGACATTCGCGGTGTTTGTATACATATATATATG 183

QY 1321 CCCGTGGCTCAACGTGAAT 1342  
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DB 182 CCCGTGGCTCAACGTGAACAT 161

RESULT 12  
BU273375/c 721 bp mRNA linear EST 09-APR-2002  
LOCUS BU273375 Y. Ogihara unpublished cDNA library, Wh\_ch Triticum  
DEFINITION aetivum cDNA clone whol1ep06 3', mRNA sequence.  
ACCESSION BU273375  
VERSION BU273375.1 GI:20098160  
KEYWORDS EST.  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum  
REFERENCE Tridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Triticum.  
1 (bases 1 to 721)  
AUTHORS Ogihara, Y. and Murai, K.  
Expressed genes in Triticum aestivum  
Unpublished (2002)  
COMMENT Contact: Tadasu Shin-i  
Center For Genetic Resource Information  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: tehin@genes.nig.ac.jp.  
Location/Qualifiers  
1..721  
/organism="Triticum aestivum"  
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ORIGIN  
Query Match 26.3%; Score 353.8; DB 12; Length 721;  
Best Local Similarity 97.4%; Pred. No. 9e-93;  
Matches 370; Conservative 0; Mismatches 8; Indels 2; Gaps 1;

QY 961 GAACATCGCATGACAGAGCGCGCTTTCTCGGTATACCTCCAGCAGACTGCG 1020  
DB 383 GAACATCGCATGACAGAGCGCGCTTTCTCGGTATACCTCCAGCAGACTGCG 324

QY 1021 GTCGTGTATGCCCTTACAGAGTAAGAACAGAGCGGCTTTGTTACAGGCAAGAGAGAA 1080  
DB 323 GTCGTGTATGCCCTTACAGAGTAAGAACAGAGCGGCTTTGTTACAGGCAAGAGAGAA 264

QY 1081 CTCAGAGAGCTCGGTATCGGTAGAGGAAGAGAGCGGCGGAGAGCTGCTCAAG 1140  
DB 263 CTCAGAGAGCTCGGTATCGGTAGAGGAAGAGAGCGGCGGAGAGCTGCTCAAG 204

QY 1141 CGCCATGACTGGAGAGGAGTCTGCTCTTCCAGATCCAGAGAGAGAGATGATAG 1200  
DB 203 CGCCATGACTGGAGAGGAGTCTGCTCTTCCAGATCCAGAGAGAGAGATGATAG 144

QY 1201 GTAGCTTGTGGTGGCGCTCGAAGAAATGAGAGGCGCTGGGTTTGTGTGCTGCA 1260  
DB 143 GTAGCTTGTGGTGGCGCTCGAAGAAATGAGAGGCGCTGGGTTTGTGTGCTGCA 84

QY 1261 CTGAACCTCTCTCTATCTTGACATTCGCGGTGTTTGTATACATATATATATG 1320  
DB 83 CT--ACCTCTCTCTATCTTGACATTCGCGGTGTTTGTATACATATATATATG 26

QY 1321 CCCGTGGCTCAACGTGAAT 1340  
DB 25 CCCGTGGCTCAACANAA 6  
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RESULT 13

LOCUS	CD934119	527 bp	mRNA	linear	EST 15-JUL-2003
DEFINITION	CD934119	GR45.123A24F010723	GR45	Triticum aestivum	CDNA clone GR45123A24.
ACCESSION	CD934119	mRNA sequence.			
VERSION	CD934119				
KEYWORDS	CD934119.1	GI:32781863			
SOURCE	EST.				
ORGANISM	Triticum aestivum (bread wheat)				
	Triticum aestivum				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.				
REFERENCE	1 (bases 1 to 527)				
AUTHORS	Genoplatane.				
TITLE	Genoplatane, a major partnership french program in plant genomics				
JOURNAL	Unpublished (2003)				
COMMENT	Contact: Genoplatane				
	Genoplatane				
	93, rue Henri Rochefort 91025 EVRY CEDEX France				
	Tel: 33 1 69 47 54 00				
	Fax: 33 1 69 47 54 10				
	This sequence has been generated in the framework of the french plant genomics programme 'Genoplatane' ( <a href="http://www.genoplatane.com">http://www.genoplatane.com</a> and <a href="http://genoplatane-info.inbio.gen.fr">http://genoplatane-info.inbio.gen.fr</a> ).				

FEATURES	Location/Qualifiers
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pollination)"
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## ORIGIN

Query Match	25.9%	Score 347.6;	DB 14;	length 527;
Best Local Similarity	96.2%	Pred. No. 5.4e-91;		
Matches 356;	Conservative	0;	Mismatches 14;	Indels 0;
				Gaps 0;

QY	961	AAACATCCGCATGACAAACAGGCGCGGCTCTTCTCGGATGACATCCGACGAACTGCG	1020
Db	135	GAACATCCGCATGACAAATAGGCGCGCTCTTCTTGGATGACATCTCTTCAGAACTGCG	194
QY	1021	GTCTGTATGCTCTTACAGAGTAAAGAACACAGCGGCTTGTTCAGAGCAAGAGAGAA	1080
Db	195	GTCTGTATGCTCTTACAGAGTAAAGAACACAGCGGCTTGTTCAGAGCAAGAGAGAA	254
QY	1081	CTCCAGAGAGCTCGTGATCGTGACGGAAGGACGGGCAAGCGGCGAGGCTGCTCCAA	1140
Db	255	CTCCAGAGAGCTCGTGATCGTGACGGAAGGACGGGCAACTGCGTGAGCTGCTCAA	314
QY	1141	CGGCATGACTGAGAGGGGATGCTGCTCTTCCCAATGCCAGAGAGAGCAAGATGATAG	1200
Db	315	CGGCATGACTGAGAGGGGATGCTGCTCTTCCCGATGCCAGAGAGATCGAATGATAG	374
QY	1201	GTACTTGTGTGTAGCGCTCGAAAGAAATGACGGGCTGAGGATGTTGTGTGCTGCA	1260
Db	375	GTACTTGTGTGTAGCGCTCGAAAGAAATGACGGGCTGAGGATGTTGTGTGCTGCA	434
QY	1261	CTGAACCTCTCTCTATCTTGCACATTCGGGTTGTTTTGTACATATACTAAATATG	1320
Db	435	CTTAACCTCTCTCTATCTTGCACATTCGGGTTGTTTTGTACATATACTAAATATG	494
QY	1321	CCCGTGCGCT	1330
Db	495	CCCGTGCGCT	504

RESULT 14				
CD899313				
LOCUS	CD899313	532 bp	mRNA	linear
DEFINITION	G174.111021F010825 G174	Triticum aestivum	CDNA clone G17411021,	

ACCESSION	RNA sequence.
VERSION	CD899913
KEYWORDS	CD899913.1 GI:32673641
SOURCE	EST.
ORGANISM	Triticum aestivum (bread wheat)
REFERENCE	Triticum aestivum
AUTHORS	Triticum aestivum
TITLE	Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
JOURNALT	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
COMMENT	Poidea; Triticeae; Triticum.
	1 (bases 1 to 532)
	Genopante.
	Genopante, a major partnership french program in plant genomics
	Unpublished (2003)
	Contact: Genopante
	Genopante
	93, rue Henri Rochefort 91025 EVRY CEDEX France
	Tel: 33 1 69 47 54 00
	Fax: 33 1 69 47 54 10
	This sequence has been generated in the framework of the french
	plant genomics programme 'Genopante' ( <a href="http://www.genopante.com">http://www.genopante.com</a>
	and <a href="http://genopante-info.infobiogen.fr">http://genopante-info.infobiogen.fr</a> ).
FEATURES	Location/Qualifiers

FEATURES	Location/Qualifiers
source	1. .532

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/db_xref="taxon:565"
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/tissue_type="grain (174 degrees per day after
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ORIGIN

Query Match	25.9%	Score 347.6	DB 14	Length 532
Best Local Similarity	96.2%	Pred No. 5	4e-91	
Matches 356	Conservative 0	Mismatches 14	Indels 0	Gaps 0

[illegible]

RESULT	15
LOCUS	CD897227
DEFINITION	CD897227 CD897227 565 bp mRNA linear EST 14-JUN-2003 G174.105D15P010823 G174 Triticum aestivum cDNA clone G174105D15, mRNA sequence.
ACCESSION	CD897227
VERSION	CD897227.1 GI:32671555

KEYWORDS EST.  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticaceae; Triticum.  
REFERENCE 1 (bases 1 to 565)  
AUTHORS Genoplatte.  
TITLE Genoplatte, a major partnership french program in plant genomics  
JOURNAL Unpublished (2003)  
COMMENT Contact: Genoplatte  
Genoplatte  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>  
and <http://genoplatte-info.infobiogen.fr>).  
Location/Qualifiers  
1..565  
/organism="Triticum aestivum"  
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/db\_xref="taxon:4565"  
/clone="G174105D15"  
/tissue\_type="grain (174 degrees per day after  
pollination)"  
/clone\_id="G174"

ORIGIN

Query Match 25.9%; Score 347.6; DB 14; Length 565;  
Best Local Similarity 96.2%; Pred. No. 5.6e-91;  
Matches 356; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 961 GAACATCCGATGACACAGCGCGCTCTTCTCGATGATCCAGCAACTGCG 1020  
DB 170 GAACATCCGATGACATAGCGCGCTCTTCTGATGATCTGCAAGACTGCG 229  
QY 1021 GTCGTATGCCCTTACAGAGTAAGACGAGCGGCTTGTACAGGCAAGAGAGAA 1080  
DB 230 GTCGTATGCCCTTACAGAGTAAGACGAGCGGCTTGTACAGGCAAGAGAGAA 289  
QY 1081 CTCGAGAGAGCTCGATCGATCGAGCAAGCAAGCGGCAAGCGGCAAGCTGCTCAAG 1140  
DB 290 CTCGAGAGAGCTCGATCGATCGAGCAAGCAAGCGGCAAGCTGCTGAGGCTGCTAAG 349  
QY 1141 CGCCATGACTGGAGGAGATCGCTCTTCCCAAGATGCCAGAGAGAGATGATAG 1200  
DB 350 CGCCATGACTGGAGGAGATCGCTCTTCCCAAGATGCCAGAGAGATGATGATAG 409  
QY 1201 GTAGCTTGTGTGAGCGCTCGAAGAAATGACGCGGCTGAGTGTGTGCTGCA 1260  
DB 410 GTAGCTTGTGTGAGCGCTCGAAGAAATGACGCGGCTGAGTGTGTGCTGCA 469  
QY 1261 CTGAACCTCTCTCCATCTTGACATTCGCGGTGTTTGTACATATACTAATAATTG 1320  
DB 470 CTGAACCTCTCTCCATCTTGACATTCGCGGTGTTTGTACATATACTAATAATTG 529  
QY 1321 CCCGTGCGCT 1330  
DB 530 CCCGTGCGCT 539